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## SEQUENCE LISTING

## (I) GENERAL INFORMATION:

(i) APPLICANT: (Other than US) THE WALTER AND ELIZA HALL INSTITUTE OF  
MEDICAL RESEARCH  
(US Only)

(ii) TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC AGENTS

(iii) NUMBER OF SEQUENCES: 49

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: DAVIES COLLISON CAVE  
(B) STREET: 1 LITTLE COLLINS STREET  
(C) CITY: MELBOURNE  
(D) STATE: VICTORIA  
(E) COUNTRY: AUSTRALIA  
(F) ZIP: 3000

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: PCT INTERNATIONAL  
(B) FILING DATE: 31-OCT-1997

(vi) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: PO5117  
(B) FILING DATE: 14-FEB-1997

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: PO 3384  
(B) FILING DATE: 01-NOV-1996

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: HUGHES DR, E JOHN L  
(C) REFERENCE/DOCKET NUMBER: EJH/EK

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: +61 3 9254 2777  
(B) TELEFAX: +61 3 9254 2770

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## (2) INFORMATION FOR SEQ ID NO:1:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CACGCCGCCC ACGTGAAGGC

20

## (2) INFORMATION FOR SEQ ID NO:2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

TTCGCCAATG ACAAGACGCT

20

## (2) INFORMATION FOR SEQ ID NO:3:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1236 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..636

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

```

CGAGGCTCAA GCTCCGGGCG GATTCTGCCT GCCGCTCTCG CTCCTTGGGG TCTGTTGGCC -101
GGCCTGTGCC ACCCGGACGC CCGGCTCACT GCCTCTGTCT CCCCATCAG CCGAGCCCCG -41
GACGCTATGG CCCACCCCTC CAGCTGGCCC CTCGAGTAGG -1

ATG GTA GCA CGC AAC CAG GTG GCA GCC GAC AAT GCG ATC TCC CCG GCA 48
Met Val Ala Arg Asn Gln Val Ala Ala Asp Asn Ala Ile Ser Pro Ala
1 5 10 15

GCA GAG CCC CGA CGG CGG TCA GAG CCC TCC TCG TCC TCG TCT TCG TCC 96
Ala Glu Pro Arg Arg Ser Glu Pro Ser Ser Ser Ser Ser Ser Ser
20 25 30

TCG CCA GCG GCC CCC GTG CGT CCC CGG CCC TGC CCG GCG GTC CCA GCC 144

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Ser	Pro	Ala	Ala	Pro	Val	Arg	Pro	Arg	Pro	Cys	Pro	Ala	Val	Pro	Ala		
		35					40					45					
CCA	GCC	CCT	GGC	GAC	ACT	CAC	TTC	CGC	ACC	TTC	CGC	TCC	CAC	TCC	GAT	192	
Pro	Ala	Pro	Gly	Asp	Thr	His	Phe	Arg	Thr	Phe	Arg	Ser	His	Ser	Asp		
		50				55					60						
TAC	CGG	CGC	ATC	ACG	CGG	ACC	AGC	GCG	CTC	CTG	GAC	GCC	TGC	GGC	TTC	240	
Tyr	Arg	Arg	Ile	Thr	Arg	Thr	Ser	Ala	Leu	Leu	Asp	Ala	Cys	Gly	Phe		
		65			70				75					80			
TAT	TGG	GGA	CCC	CTG	AGC	GTG	CAC	GGG	GCG	CAC	GAG	CGG	CTG	CGT	GCC	288	
Tyr	Trp	Gly	Pro	Leu	Ser	Val	His	Gly	Ala	His	Glu	Arg	Leu	Arg	Ala		
				85				90						95			
GAG	CCC	GTG	GGC	ACC	TTC	TTG	GTG	CGC	GAC	AGT	CGT	CAA	CGG	AAC	TCC	336	
Glu	Pro	Val	Gly	Thr	Phe	Leu	Val	Arg	Asp	Ser	Arg	Gln	Arg	Asn	Cys		
		100						105				110					
TTC	TTC	GCG	CTC	AGC	CTG	AAG	ATG	GCT	TCG	GCC	CCC	ACG	AGC	ATC	CGC	384	
Phe	Phe	Ala	Leu	Ser	Val	Lys	Met	Ala	Ser	Gly	Pro	Thr	Ser	Ile	Arg		
		115				120						125					
GTG	CAC	TTC	CAG	GCC	GCG	CGC	TTC	CAC	TTG	GAC	GGC	AGC	CGC	GAG	ACC	432	
Val	His	Phe	Gln	Ala	Gly	Arg	Phe	His	Leu	Asp	Gly	Ser	Arg	Glu	Thr		
		130				135					140						
TTC	GAC	TGC	CTT	TTC	GAG	CTG	CTG	GAG	CAC	TAC	GTG	GCG	GCG	CCG	CGC	480	
Phe	Asp	Cys	Leu	Phe	Glu	Leu	Leu	Glu	His	Tyr	Val	Ala	Ala	Pro	Arg		
		145			150					155					160		
CGC	ATG	TTG	GGG	GCC	CCG	CTG	CGC	CAG	CGC	CGC	GTG	CGG	CCG	CTG	CAG	528	
Arg	Met	Leu	Gly	Ala	Pro	Leu	Arg	Gln	Arg	Arg	Val	Arg	Pro	Leu	Gln		
				165				170						175			
GAG	CTG	TGT	CGC	CAG	CGC	ATC	GTG	GCC	GCC	GTG	GGT	CGC	GAG	AAC	CTG	576	
Glu	Leu	Cys	Arg	Gln	Arg	Ile	Val	Ala	Ala	Val	Gly	Arg	Glu	Asn	Leu		
			180					185					190				
GCG	CGC	ATC	CCT	CTT	AAC	CCG	GTA	CTC	CGT	GAC	TAC	CTG	AGT	TCC	TTC	624	
Ala	Arg	Ile	Pro	Leu	Asn	Pro	Val	Leu	Arg	Asp	Tyr	Leu	Ser	Ser	Phe		
		195				200						205					
CCC	TTC	CAG	ATC	TGA	CCGGCTG	CCGCTGTGCC	GCAGCATTAA	GTGGGGGCGC								676	
Pro	Phe	Gln	Ile	*													
		210															
CTTATTATTT	CTTATTATTA	ATTATTATTA	TTTTTCTGGA	ACCACGTGGG	AGCCCTCCCU											736	
GCCTGGGTCTG	GAGGGAGTGG	TTGTGGAGGG	TGAGATGCCT	CCCACCTCTG	GCTGGAGACC											796	
TCATCCCAAC	TCTCAGGGGT	GGGGGTGCTC	CCCTCCTGCT	GCTCCCTCCG	GGTCCCCCCT											856	
GGTTGTAGCA	GCTGTGTCT	GGGGCCAGGA	CCTGAATTC	ACTCCTACCT	CTCCATGTTT											916	
ACATATTCCC	AGTATCTTTG	CACAAACCAG	GGGTGCGGGA	GGGTCTCTGG	CTTCATTTT											976	
CTGCTGTGCA	GAATATCCTA	TTTTATATTT	TTACAGCCAG	TTTAGGTAAT	AAACTTTATT											1036	
ATGAAAGTTT	TTTTTTAAAA	GAARAAAAAA	AAAAAAAAA													1075	

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 212 amino acids

SUBSTITUTE SHEET (Rule 26)

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(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```

Met Val Ala Arg Asn Gln Val Ala Ala Asp Asn Ala Ile Ser Pro Ala
 1           5           10           15
Ala Glu Pro Arg Arg Arg Ser Glu Pro Ser Ser Ser Ser Ser Ser Ser
          20           25           30
Ser Pro Ala Ala Pro Val Arg Pro Arg Pro Cys Pro Ala Val Pro Ala
          35           40           45
Pro Ala Pro Gly Asp Thr His Phe Arg Thr Phe Arg Ser His Ser Asp
          50           55           60
Tyr Arg Arg Ile Thr Arg Thr Ser Ala Leu Leu Asp Ala Cys Gly Phe
          65           70           75           80
Tyr Trp Gly Pro Leu Ser Val His Gly Ala His Glu Arg Leu Arg Ala
          85           90           95
Glu Pro Val Gly Thr Phe Leu Val Arg Asp Ser Arg Gln Arg Asn Cys
          100          105          110
Phe Phe Ala Leu Ser Val Lys Met Ala Ser Gly Pro Thr Ser Ile Arg
          115          120          125
Val His Phe Gln Ala Gly Arg Phe His Leu Asp Gly Ser Arg Glu Thr
          130          135          140
Phe Asp Cys Leu Phe Glu Leu Leu Glu His Tyr Val Ala Ala Pro Arg
          145          150          155          160
Arg Met Leu Gly Ala Pro Leu Arg Gln Arg Arg Val Arg Pro Leu Gln
          165          170          175
Glu Leu Cys Arg Gln Arg Ile Val Ala Ala Val Gly Arg Glu Asn Leu
          180          185          190
Ala Arg Ile Pro Leu Asn Pro Val Leu Arg Asp Tyr Leu Ser Ser Phe
          195          200          205
Pro Phe Gln Ile
          210

```

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1121 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:  
 (A) NAME/KEY: CDS  
 (B) LOCATION: 223..819

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GCGATCTGTG GGTGACAGTG TCTGCGAGAG ACTTTGCCAC ACCATTCTGC CGGAATTTGG	60
AGAAAAAGAA CCAGCCGCTT CCAGTCCCTT CCCCCTCCGC CACCATTTCG GACACCCCTGC	120
ACACTCTCGT TTTGGGGTAC CCTGTGACTT CCAGGCAGCA CGCGAGGTCC ACTGGCCCCA	180
GCTCGGGCGA CCAGCTGTCT GGGACGTGTT GACTCATCTC CC ATG ACC CTG CGG	234
Met Thr Leu Arg	
1	
TGC CTG GAG CCC TCC GGG AAT GGA GCG GAC AGG ACC CGG AGC CAG TGG	282
Cys Leu Glu Pro Ser Gly Asn Gly Ala Asp Arg Thr Arg Ser Gln Trp	
5 10 15 20	
GGG ACC GCG GGG TTG CCG GAG GAA CAG TCC CCC GAG GCG GCG CGT CTG	330
Gly Thr Ala Gly Leu Pro Glu Glu Gln Ser Pro Glu Ala Ala Arg Leu	
25 30 35	
GCG AAA GCC CTG CGC GAG CTC AGT CAA ACA GGA TGG TAC TGG GGA AGT	378
Ala Lys Ala Leu Arg Glu Leu Ser Gln Thr Gly Trp Tyr Trp Gly Ser	
40 45 50	
ATG ACT GTT AAT GAA GCC AAA GAG AAA TTA AAA GAG GCT CCA GAA GGA	426
Met Thr Val Asn Glu Ala Lys Glu Lys Leu Lys Glu Ala Pro Glu Gly	
55 60 65	
ACT TTC TTG ATT AGA GAT AGT TCG CAT TCA GAC TAC CTA CTA ACT ATA	474
Thr Phe Leu Ile Arg Asp Ser Ser His Ser Asp Tyr Leu Leu Thr Ile	
70 75 80	
TCC GTT AAG ACG TCA GCT GGA CCG ACT AAC CTG CGG ATT GAG TAC CAA	522
Ser Val Lys Thr Ser Ala Gly Pro Thr Asn Leu Arg Ile Glu Tyr Gln	
85 90 95 100	
GAT GGG AAA TTC AGA TTG GAT TCT ATC ATA TGT GTC AAG TCC AAG CTT	570
Asp Gly Lys Phe Arg Leu Asp Ser Ile Ile Cys Val Lys Ser Lys Leu	
105 110 115	
AAA CAG TTT GAC AGT GTG GTT CAT CTG ATT GAC TAC TAT GTC CAG ATG	618
Lys Gln Phe Asp Ser Val Val His Leu Ile Asp Tyr Tyr Val Gln Met	
120 125 130	
TGC AAG GAT AAA CGG ACA GGC CCA GAA GCC CCA CGG AAT GCG ACT GTT	666
Cys Lys Asp Lys Arg Thr Gly Pro Glu Ala Pro Arg Asn Gly Thr Val	
135 140 145	
CAC CTG TAC CTG ACC AAA CCT CTG TAT ACA TCA GCA CCC ACT CTG CAG	714
His Leu Tyr Leu Thr Lys Pro Leu Tyr Thr Ser Ala Pro Thr Leu Gln	
150 155 160	
CAT TTC TGT CGA CTC GCC ATT AAC AAA TGT ACC GGT ACG ATC TGG GGA	762
His Phe Cys Arg Leu Ala Ile Asn Lys Cys Thr Gly Thr Ile Trp Gly	
165 170 175 180	
CTG CCT TTA CCA ACA AGA CTA AAA GAT TAC TTG GAA GAA TAT AAA TTC	810
Leu Pro Leu Pro Thr Arg Leu Lys Asp Tyr Leu Glu Glu Tyr Lys Phe	
185 190 195	
CAG GTA TAAGTATTTT TCTCTCTTTT TCGTTTTTTT TTAAAAAAA AAAACACAT	866
Gln Val	
GCCTCATATA GACTATCTCC GAATGCAGCT ATGTGAAAGA GAACCCAGAG GCCCTCCTCT	926
GGATAACTGC GCAGAACTCT CTCTTAAGGA CAGTTGGGCT CAGTCTAACT TAAAGGTGTG	986

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AAGATGTAGC TAGGTATTTT AAAGTTCCCC TTAGGTAGTT TTAGCTGAAT GATGCTTTCT 1046  
 TTCCTATGGC TGCTCAAGAT CAAATGGCCC TTTTAAATGA AACAAAACAA AACAAAACAA 1106  
 AAAAAAAAAA AAAAA 1121

## (2) INFORMATION FOR SEQ ID NO:6:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 198 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Thr Leu Arg Cys Leu Glu Pro Ser Gly Asn Gly Ala Asp Arg Thr  
 1 5 10 15  
 Arg Ser Gln Trp Gly Thr Ala Gly Leu Pro Glu Glu Gln Ser Pro Glu  
 20 25 30  
 Ala Ala Arg Leu Ala Lys Ala Leu Arg Glu Leu Ser Gln Thr Gly Trp  
 35 40 45  
 Tyr Trp Gly Ser Met Thr Val Asn Glu Ala Lys Glu Lys Leu Lys Glu  
 50 55 60  
 Ala Pro Glu Gly Thr Phe Leu Ile Arg Asp Ser Ser His Ser Asp Tyr  
 65 70 75 80  
 Leu Leu Thr Ile Ser Val Lys Thr Ser Ala Gly Pro Thr Asn Leu Arg  
 85 90 95  
 Ile Glu Tyr Gln Asp Gly Lys Phe Arg Leu Asp Ser Ile Ile Cys Val  
 100 105 110  
 Lys Ser Lys Leu Lys Gln Phe Asp Ser Val Val His Leu Ile Asp Tyr  
 115 120 125  
 Tyr Val Gln Met Cys Lys Asp Lys Arg Thr Gly Pro Glu Ala Pro Arg  
 130 135 140  
 Asn Gly Thr Val His Leu Tyr Leu Thr Lys Pro Leu Tyr Thr Ser Ala  
 145 150 155 160  
 Pro Thr Leu Gln His Phe Cys Arg Leu Ala Ile Asn Lys Cys Thr Gly  
 165 170 175  
 Thr Ile Trp Gly Leu Pro Leu Pro Thr Arg Leu Lys Asp Tyr Leu Glu  
 180 185 190  
 Glu Tyr Lys Phe Gln Val  
 195

## (2) INFORMATION FOR SEQ ID NO:7:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2187 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA

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## (ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 18..695

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CGCTGGCTCC GTCCGCC ATG GTC ACC CAC AGC AAG TTT CCC GCC GCC GGG	50
Met Val Thr His Ser Lys Phe Pro Ala Ala Gly	
1 5 10	
ATG AGC CGC CCC CTG GAC ACC AGC CTG CGC CTC AAG ACC TTC AGC TCC	98
Met Ser Arg Pro Leu Asp Thr Ser Leu Arg Leu Lys Thr Phe Ser Ser	
15 20 25	
AAA AGC GAG TAC CAG CTG GTG GTG AAC GCC GTG CGC AAG CTG CAG GAG	146
Lys Ser Glu Tyr Gln Leu Val Val Asn Ala Val Arg Lys Leu Gln Glu	
30 35 40	
AGC GGA TTC TAC TGG AGC GCC GTG ACC GGC GGC GAG GCG AAC CTG CTG	194
Ser Gly Phe Tyr Trp Ser Ala Val Thr Gly Gly Glu Ala Asn Leu Leu	
45 50 55	
CTC AGC GCC GAG CCC GCG GGC ACC TTT CTT ATC CCC GAC AGC TCG GAC	242
Leu Ser Ala Glu Pro Ala Gly Thr Phe Leu Ile Arg Asp Ser Ser Asp	
60 65 70 75	
CAG CGC CAC TTC TTC ACG TTG AGC GTC AAG ACC CAG TCG GGG ACC AAG	290
Gln Arg His Phe Phe Thr Leu Ser Val Lys Thr Gln Ser Gly Thr Lys	
80 85 90	
AAC CTA CGC ATC CAG TGT GAG GGG GGC AGC TTT TCG CTG CAG AGT GAC	338
Asn Leu Arg Ile Gln Cys Glu Gly Gly Ser Phe Ser Leu Gln Ser Asp	
95 100 105	
CCC CGA AGC ACG CAG CCA GTT CCC CGC TTC GAC TGT GTA CTC AAG CTG	386
Pro Arg Ser Thr Gln Pro Val Pro Arg Phe Asp Cys Val Leu Lys Leu	
110 115 120	
GTG CAC CAC TAC ATG CCG CCT CCA GGG ACC CCC TCC TTT TCT TTG CCA	434
Val His His Tyr Met Pro Pro Pro Gly Thr Pro Ser Phe Ser Leu Pro	
125 130 135	
CCC ACG GAA CCC TCG TCC GAA GTT CCG GAG CAG CCA CCT GCC CAG GCA	482
Pro Thr Glu Pro Ser Ser Glu Val Pro Glu Gln Pro Pro Ala Gln Ala	
140 145 150 155	
CTC CCC GGG AGT ACC CCC AAG AGA GCT TAC TAC ATC TAT TCT GGG GGC	530
Leu Pro Gly Ser Thr Pro Lys Arg Ala Tyr Tyr Ile Tyr Ser Gly Gly	
160 165 170	
GAG AAG ATT CCG CTG GTA CTG AGC CGA CCT CTC TCC TCC AAC GTG GCC	578
Glu Lys Ile Pro Leu Val Leu Ser Arg Pro Leu Ser Ser Asn Val Ala	
175 180 185	
ACC CTC CAG CAT CTT TGT CCG AAG ACT GTC AAC GGC CAC CTG GAC TCC	626
Thr Leu Gln His Leu Cys Arg Lys Thr Val Asn Gly His Leu Asp Ser	
190 195 200	
TAT GAG AAA GTG ACC CAG CTG CCT GGA CCC ATT CGG GAG TTC CTG GAT	674
Tyr Glu Lys Val Thr Gln Leu Pro Gly Pro Ile Arg Glu Phe Leu Asp	
205 210 215	
CAG TAT GAT GCT CCA CTT TAAGGAGCAA AAGGGTCAGA GGGGGGCTG	722
Gln Tyr Asp Ala Pro Leu	
220 225	

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GGTCGGTCGG TCGCCTCTCC TCCGAGGCAC ATGGCACAAG CACAAAAATC CAGCCCCAAC 782
GGTCGGTAGC TCCAGTGAG CCAGGGGCAG ATTGGCTTCT TCTCAGGCC CTCCACTCCC 842
GCAGAGTAGA GCTGGCAGGA CCTGGAATTC GTCTGAGGGG AGGGGGAGCT GCCACCTGCT 902
TTCCCCCCTC CCCCAGCTCC AGCTTCTTTC AAGTGGAGCC AGCCGGCCTG GCCTGGTGGG 962
ACAATACCTT TGACAAGCGG ACTCTCCCTC CCCCTTCCTC CACACCCCTC CTGCTTCCCA 1022
AGGGAGGTGG GGACACCTCC AAGTGTGAA CTTAGAACTG CAAGGGGAAT CTTCAAACCT 1082
TCCCGCTGGA ACTTGTTTGC GCTTTGATTT GTTTGATCA AGAGCAGGCA CCTGGGGGAA 1142
GGATGGAAGA GAAAAGGGTG TGTGAAGGGT TTTTATGCTG GCCAAAGAAA TAACCACTCC 1202
CACTGCCCAA CCTAGGTGAG GAGTGGTGGC TCCTGGCTCT GGGGAGAGTG GCAAGGGGTG 1262
ACCTGAAGAG AGCTATACTG GTGCCAGGCT CCTCTCCATG GGGCAGCTAA TGAAACCTCG 1322
CAGATCCCTT GCACCCCAAG ACCCTCCCTG TTGTGAAGAG GCAGTAGCAT TTAGAAGGGA 1382
GACAGATGAG GCTGGTGAGC TGGCCGCCCT TTCCAACACC GAAGGGAGGC AGATCAACAG 1442
ATGAGCCATC TTGGAGCCCA GGTTCCTCTT GGAGCAGATG GAGGGTCTCT CTTTGTCTCT 1502
CCTATGTGGG GCTAGGAGAC TCGCCTTAAA TGCCCTCTGT CCCAGGGATG GGGATTGGCA 1562
CACAAGGAGC CAAACACAGC CAATAGGCAG AGAGTTGAGG GATTACCCA GGTGGCTACA 1622
GGCCAGGGGA AGTGGCTGCA GGGGAGAGAC CCAGTCACTC CAGGAGACTC CTGAGTTAAC 1682
ACTGGGAAGA CATTGGCCAG TCCTAGTCAT CTCTCGGTCA GTAGGTCCGA GAGCTTCCAG 1742
GCCCTGCACA GCCCTCCTTT CTCACCTGGG GGGAGGCAGG AGGTGATGGA GAAGCCTTCC 1802
CATGCCGCTC ACAGGGGCCCT CACGGGAATG CAGCAGCCAT GCAATTACCT GGAAGTGGTC 1862
CTGTGTTGGG GAGAAACAAG TTTTCTGAAG TCAGGTATGG GGCTGGGTGG GCCAGCTGTG 1922
TGTTGGGGTG GCTTTTTTCT CTCTGTTTTG AATAATGTTT ACAATTTGCC TCAATCACTT 1982
TTATAAAAAA CCACCTCCAG CCGCCCCCTC TCCCCTCACTA GGCCTTCGAG GCTGTCTGAA 2042
GATGCTTGAA AAACCTCAAC AAATCCCAGT TCAACTCAGA CTTTGACAT ATATTTATAT 2102
TTATACTCAG AAAAGAAACA TTTCAGTAAT TTATAATBAA AGAGCACTAT TTTTAAATGA 2162
AAAAAAAAAA AAAAAAAAAA AAAAA 2187

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## (2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 225 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

```

Met Val Thr His Ser Lys Phe Pro Ala Ala Gly Met Ser Arg Pro Leu
 1           5           10           15
Asp Thr Ser Leu Arg Leu Lys Thr Phe Ser Ser Lys Ser Glu Tyr Gln
          20           25           30

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Leu Val Val Asn Ala Val Arg Lys Leu Gln Glu Ser Gly Phe Tyr Trp  
           35                          40                          45  
 Ser Ala Val Thr Gly Gly Glu Ala Asn Leu Leu Leu Ser Ala Glu Pro  
           50                          55                          60  
 Ala Gly Thr Phe Leu Ile Arg Asp Ser Ser Asp Gln Arg His Phe Phe  
           65                          70                          75                          80  
 Thr Leu Ser Val Lys Thr Gln Ser Gly Thr Lys Asn Leu Arg Ile Gln  
                           85                          90                          95  
 Cys Glu Gly Gly Ser Phe Ser Leu Gln Ser Asp Pro Arg Ser Thr Gln  
                           100                          105                          110  
 Pro Val Pro Arg Phe Asp Cys Val Leu Lys Leu Val His His Tyr Met  
           115                          120                          125  
 Pro Pro Pro Gly Thr Pro Ser Phe Ser Leu Pro Pro Thr Glu Pro Ser  
           130                          135                          140  
 Ser Glu Val Pro Glu Gln Pro Pro Ala Gln Ala Leu Pro Gly Ser Thr  
           145                          150                          155                          160  
 Pro Lys Arg Ala Tyr Tyr Ile Tyr Ser Gly Gly Glu Lys Ile Pro Leu  
                           165                          170                          175  
 Val Leu Ser Arg Pro Leu Ser Ser Asn Val Ala Thr Leu Gln His Leu  
                           180                          185                          190  
 Cys Arg Lys Thr Val Asn Gly His Leu Asp Ser Tyr Glu Lys Val Thr  
           195                          200                          205  
 Gln Leu Pro Gly Pro Ile Arg Glu Phe Leu Asp Gln Tyr Asp Ala Pro  
           210                          215                          220  
 Leu  
 225

## (2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1094 base pairs
  - (B) TYPE: nucleic acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CTCCGGCTGG	CCCCCTCTGT	AGGATGGTAG	CACACAACCA	GGTGCCAGCC	GACAATGCAG	60
TCTCCACAGC	AGCAGAGCCC	CGACGGCGGC	CAGAACCTTC	CTCCTCTTCC	TCCTCCTCGC	120
CCGCGGCCCC	CGCGCGCCCG	CGGCGGTGCC	CCGCGGTCCC	GGCCCCGGCC	CCCCGCGACA	180
CGCACTTCCG	CACATTCCGT	TGGCAGCCCG	ATTACCGGCG	CATCAGCGCG	GCCAGCGCGC	240
TCCTGGACGC	CTGCGGATTC	TACTGGGGGC	CCCTGAGCGT	GCACGGGGCG	CACGAGCGGC	300
TGCGCGCCGA	GCCCCGTGGC	ACCTTCCTGG	TGCGCGACAG	CCGCCAGCGG	AACCTGCTTTT	360
TCGCCCCCTAG	CGTGAAGATG	GCCTCGGGAC	CCACGAGCAT	CCGCGTGCAC	TTCAGGCCCC	420
CGCGCTTTCA	CCTGGATGGC	AGCCGCGAGA	GCTTCGACTG	CCTCTTCGAG	CTGCTGGAGC	480

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ACTACGTGGC GCGCCCGCGC CGCATGCTGG GGGCCCCGCT GCGCCAGCGC CGCGTGCGGC      540
CGCTGCAGGA GCTGTGCCGC CAGCGCATCG TGGCCACCGT GGGCCGCGAG AACCTGGCTC      600
GCATCCCCCT CAACCCCGTC CTCCGCGACT ACCTGAGCTC CTTCCCCCTC CAGATTTGAC      660
CGGCAGCGCC CGCCGTGCAC GCAGCATTAA CTGGGATGCC GTGTTATTTT GTTATTACTT      720
GCCTGGAACC ATGTGGGTAC CCTCCCCGGC CTGGGTGGA GGGAGCGGAT GGGTGTAGGG      780
GCGAGCGGCC TCCCGCCCTC GGCTGGAGAC GAGGCCGAG ACCCCTTC TC ACCTCTTGAG      840
GGGGTCCTCC CCTCCTGGT GCTCCCTCTG GGTCCCCCTG GTTGTGTAG CAGCTTAACT      900
GTATCTGGAG CCAGGACCTG AACTCGCACC TCCTACCTCT TCATGTTTAC ATATACCCAG      960
TATCTTTGCA CAAACCAGGG GTTGGGGGAG GGTCTCTGGC TTTATTTTTC TGCTGTGCAG     1020
AATCCTATTT TATATTTTTT AAAGTCAGTT TAGGTAATAA ACTTTATTAT GAAAGTTTTT     1080
TTTTTTAAAA AAAA                                     1094

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## (2) INFORMATION FOR SEQ ID NO:10:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 211 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

```

Met Val Ala His Asn Gln Val Ala Ala Asp Asn Ala Val Ser Thr Ala
1           5           10           15

Ala Glu Pro Arg Arg Arg Pro Glu Pro Ser Ser Ser Ser Ser Ser Ser
20           25           30

Pro Ala Ala Pro Ala Arg Pro Arg Pro Cys Pro Ala Val Pro Ala Pro
35           40           45

Ala Pro Gly Asp Thr His Phe Arg Thr Phe Arg Ser His Ala Asp Tyr
50           55           60

Arg Arg Ile Thr Arg Ala Ser Ala Leu Leu Asp Ala Cys Gly Phe Tyr
65           70           75           80

Trp Gly Pro Leu Ser Val His Gly Ala His Glu Arg Leu Arg Ala Glu
85           90           95

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Pro Val Gly Thr Phe Leu Val Arg Asp Ser Arg Gln Arg Asn Cys Phe  
 100 105 110

Phe Ala Leu Ser Val Lys Met Ala Ser Gly Pro Thr Ser Ile Arg Val  
 115 120 125

His Phe Gln Ala Gly Arg Phe His Leu Asp Gly Ser Arg Glu Ser Phe  
 130 135 140

Asp Cys Leu Phe Glu Leu Leu Glu His Tyr Val Ala Ala Pro Arg Arg  
 145 150 155 160

Met Leu Gly Ala Pro Leu Arg Gln Arg Arg Val Arg Pro Leu Gln Glu  
 165 170 175

Leu Cys Arg Gln Arg Ile Val Ala Thr Val Gly Arg Glu Asn Leu Ala  
 180 185 190

Arg Ile Pro Leu Asn Pro Val Leu Arg Asp Tyr Leu Ser Ser Phe Pro  
 195 200 205

Phe Gln Ile  
 210

## (2) INFORMATION FOR SEQ ID NO:11:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2807 base pairs  
 (B) TYPE: nucleic acid  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GGAAACCGAG GCGGGGAGAC CAGGAGGCCT TGGCCTCAGA GCTTCAGAGT CGCGTGGCAG 60  
 CAAACAGAGA AACCTGTAGA GGGCAGTGTG CGTCACCTTAG CTCAGGGAAC CTGCACGCGA 120  
 AACTCACCCG CCTTCATTCA TAAACATCGT CAGCTAGGCA CCTACTCCTG GGCTTTCAGG 180  
 ACAAACTGAA TCACGAAACC ACAGTGTCTT TAAAATAGGT CTGACCGCCT GAATCCCTGG 240  
 CCAAGGTGTG TACGGGCGAT GGGAGCCCTT GTGCAGAGAT GCTTGCAGGA GCCTTGAGCG 300  
 GCTCTGTAAG ACAGAGGCTA GGAAGACAAA GTTGGGGGCT ACAGCTTCTT GTCCTGCCCG 360  
 GGGCCTCAGT TTCTTCGGTT GCCCACGTAG GAGTGCAGAG AGTCCAGCCC CTGGGGACCC 420  
 AACCCAACCC CGCCAGTTT CCGAGGAACF CGTCCGGGAG CCGGGGCGCC CTTCCCGCAC 480  
 CCGCTTAGGC TTCCTTGAA GCCTCTGCGG TCAGGCCACC GCTTCTTGGG AAGCCCAAGC 540

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CAAGGCCAGG	CCGAGTGGCC	AACGGGAGGG	GCCCGCGCGC	GATTCTGGAG	GAGGGCGGCG	600
GCCCCACAGG	TCTCCAGGGC	TGGCTAGCCG	GGCTCCTAGA	GCGGAGACTG	CCAAGGCCTT	660
CGGGTCCCTG	GCAGGAAGGA	TCCTGGCAGG	GAGGAGTTGC	TTGGGGGGTG	GGGGGAAAG	720
GCTCCAGCGG	CGGTGGAGCT	CTGACCAGGA	GAATGCACAC	ACTCGGAGGG	GAGGAGGCGT	780
GTCAGCCCCA	AGCTAGCATC	CCACCCGGGG	AGCAGCGATG	TGGGGCGAAG	GTAGCCAGAG	840
CAAAAGAGCA	GGCACCAGGT	GACACGAAAC	AGAAGATTCC	GGGTAGAGCC	AGAACCCAG	900
AAGTCCCATT	CAGGGAAGGT	GCGAGGCGAG	AACGAGTTAG	GTGGACCCCT	TCCAGGGGCA	960
GCCAAAGAAA	TCTAAAGAGA	ACCCGAAGGA	CTTGCCCGAA	AGAGAAACCG	AAAGCGGCGG	1020
TGGGCGGGAT	CGGTGGGCGG	GCCCTCCCTG	GTTTAAAGAG	TTGATGCAGG	GGCGGGCAGC	1080
AGCAGAGAGA	ACTGGGGCGG	TGGCAGCGGC	ACGGCTCCCG	GCCCCGGAGC	ATGCGCGACA	1140
GCAGCCCGGG	AACCCCGAGC	CCCGGCGCCC	CGCCTCCCGC	CGCCAGGTGA	GCCGAGGCAG	1200
CTGCGAAGGA	GCAGGCGGGA	GGGGATGGGA	GGAAGGGGAG	CAGAGCCTGG	CAGGACTATC	1260
CTGCGAGACT	GCATGGCGGG	GTGCTGGATG	CTATGCTCTT	GGCGCCCGCC	CCACCGGCTG	1320
GCCCCAGCGG	CCCCCTCGGC	GCGCGGGGCG	CCGTGAGCCC	CTCCTCTCCG	GCCCTGAGCC	1380
CGGATCGTCC	GCCCCGGGTT	CAGTTCCCGG	CGTGCCCAAT	AGGCGGCAAC	CGCGAGGCGG	1440
CAAGCCACCC	AGCGGGGACG	GCCTGGAGTC	GGGCCCCCTT	CCACGCCCCC	TTCTCCACGC	1500
GC CGGGGAG	GCAGGGCTCC	ACCGCCAGTC	TGGAAGGGTT	CCACATACAG	GAACGGCCTA	1560
CTTCGCGAGT	GAGCCACCG	AGGCTCAGGC	TCCGGGCGGA	TTCTGCGTGT	CACCCTCGGT	1620
CCTTGGGGTC	CGCTGGCCGG	CCTGTGCCAC	CCGGACGCCC	GGTTCACTGC	CTCTCTCTCC	1680
CCCATCAGCG	CAGCCCCGGA	CGCTATGGCC	CACCCCTCCA	GCTGGCCCCCT	CGAGTAGGAT	1740
GGTAGCACGT	AACCAGGTGG	AAGCCGACAA	TGCGATCTCC	CCGGCATCAG	AGCCCCGACG	1800
GCGGCCAGAG	CCATCTTCGT	CCTCGTCTTC	GTCTCTCGCG	GCGGCCCCCG	CGCGTCCCGG	1860
GCCCTGCCCC	GTGGTCCCGG	CCCCGGCTCC	GGGCGACACT	CACTTCCGCA	CCCTCCCGCT	1920
CCACTCTGAT	TACCGGCGCA	TCACCGGAC	CAGCGCTCTC	CTGGACGCGT	GCGGCTTCTA	1980
CTGGGGACCC	CTGAGCGTGC	ATGGGGCGCA	CGAACGGCTG	CGTTCCGAAC	CCGTGGGCAC	2040
CTTCTTGGTG	CGCGACAGTC	GCCAGCGGAA	CTGCTTCTTC	GCGCTCAGCG	TGAAGATGGC	2100
TTGCGGCCCC	ACGAGCATTC	GTGTGCACTT	CCAGGCCGGC	CGCTTCCACC	TGGACGGCAA	2160
CCGCGAGACC	TTGAGCTGCC	TCTTCGAGCT	GCTGGAGCAC	TACGTGGCGG	CGCCGCGCGG	2220
CATGTTGGGG	GCCCCACTGC	GCCAGCGCGG	CGTGCGGCGG	CTGCAGGAGC	TGTGTCCGCA	2280
GCGCATCGTG	GCCGCCGTGG	GTGCGGAGAA	CCTGGCAGCG	ATCCCTCTTA	ACCCGGTACT	2340
CCGTGACTAC	CTGAGTTCTT	TCCCTTCCA	GATCTGACCG	GCTGCCGCGG	TGCCCGCAGA	2400
ATTAAGTGGG	AGCGCCTTAT	TATTCCTTAT	TATTAATAT	TATTAATTTT	CTGGAACCAC	2460
GTGGGAGCCC	TCCCCGCTTA	GCTCGGAGGG	AGTGGGTGTG	GAGGGTGAGA	TCCCTCCAC	2520
TTCTGGCTGG	AGACCTTATC	CCGCTCTTCG	GGGGGCTTCC	CCTCCTGGTG	CTCCCTCCCC	2580
GTCCCCCTGG	TTGTAGCAGC	TTGTGTCTGG	GGCCAGGACC	TGAACCTCAC	GCCTACCTCT	2640
CCATGTTTAC	ATGTTCCCGAG	TATCTTTTCA	CAAACCAAGG	GTGGGGGAGG	GTCTCTGGCT	2700
TCATTTTCTT	GCTGTGCAGA	ATATTTCTAT	TTATATTTT	ACATCCAGTT	TAGATAATAA	2760
ACTTTATTAT	GAAAGTTTTT	TTTTTTAAAG	AAACAAAGAT	TTCTAGA		2807

(2) INFORMATION FOR SEQ ID NO:12:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 212 amino acids

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(B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met	Val	Ala	Arg	Asn	Gln	Val	Glu	Ala	Asp	Asn	Ala	Ile	Ser	Pro	Ala	1	5	10	15
Ser	Glu	Pro	Arg	Arg	Arg	Pro	Glu	Pro	Ser	Ser	Ser	Ser	Ser	Ser	Ser	20	25	30	
Ser	Pro	Ala	Ala	Pro	Ala	Arg	Pro	Arg	Pro	Cys	Pro	Val	Val	Pro	Ala	35	40	45	
Pro	Ala	Pro	Gly	Asp	Thr	His	Phe	Arg	Thr	Phe	Arg	Ser	His	Ser	Asp	50	55	60	
Tyr	Arg	Arg	Ile	Thr	Arg	Thr	Ser	Ala	Leu	Leu	Asp	Ala	Cys	Gly	Phe	65	70	75	80
Tyr	Trp	Gly	Pro	Leu	Ser	Val	His	Gly	Ala	His	Glu	Arg	Leu	Arg	Ser	85	90	95	
Glu	Pro	Val	Gly	Thr	Phe	Leu	Val	Arg	Asp	Ser	Arg	Gln	Arg	Asn	Cys	100	105	110	
Phe	Phe	Ala	Leu	Ser	Val	Lys	Met	Ala	Ser	Gly	Pro	Thr	Ser	Ile	Arg	115	120	125	
Val	His	Phe	Gln	Ala	Gly	Arg	Phe	His	Leu	Asp	Gly	Asn	Arg	Glu	Thr	130	135	140	
Phe	Asp	Cys	Leu	Phe	Glu	Leu	Leu	Glu	His	Tyr	Val	Ala	Ala	Pro	Arg	145	150	155	160
Arg	Met	Leu	Gly	Ala	Pro	Leu	Arg	Gln	Arg	Arg	Val	Arg	Pro	Leu	Gln	165	170	175	
Glu	Leu	Cys	Arg	Gln	Arg	Ile	Val	Ala	Ala	Val	Gly	Arg	Glu	Asn	Leu	180	185	190	

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Ala Arg Ile Pro Leu Asn Pro Val Leu Arg Asp Tyr Leu Ser Ser Phe  
 195 200 205

Pro Phe Gln Ile  
 210

## (2) INFORMATION FOR SEQ ID NO:13:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1611 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 263..1529

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CGAATTCGG GCGGGCTGTG TGAGTCTGTG AGTGAAGGC GCGCGGCTC TTTTGTCTGA 60  
 GTGTGACCCG GTGGCTTTGT TCCAGGCATT CCGGTGATTT CCTCCGGGCA GTCCGCAGAA 120  
 GCGCAGCGG CCGCCCGCGC TCTCTCTGCA GTCTCCACAC CCGGAGAGC CTGAGCCCGC 180  
 GTCACGCCCC TCAGCCCCCG CTGAGTCCCT TCTCTGTTGT CCGTCCGAA TCGAGTTCCC 240  
 GGAATCAGAC GGTGCCCCAT AG ATG GCC AGC TTT CCC CCG AGG GTT AAC GAG 292  
 Met Ala Ser Phe Pro Pro Arg Val Asn Glu  
 1 5 10  
 AAA GAG ATC GTG AGA TCA CGT ACT ATA GGG GAA CTC TTG GCT CCA GCA 340  
 Lys Glu Ile Val Arg Ser Arg Thr Ile Gly Glu Leu Leu Ala Pro Ala  
 15 20 25  
 GCT CCT TTT GAC AAG AAA TGT GGT GGT GAG AAC TGG ACG GTT GCT TTT 388  
 Ala Pro Phe Asp Lys Lys Cys Gly Gly Glu Asn Trp Thr Val Ala Phe  
 30 35 40

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GCT CCT GAT GGT TCC TAC TTT GCG TGG TCA CAA GGA TAT CGC ATA GTG	436
Ala Pro Asp Gly Ser Tyr Phe Ala Trp Ser Gln Gly Tyr Arg Ile Val	
45 50 55	
AAG CTT GTC CCG TGG TCC CAG TGC CGT AAG AAC TTT CTT TTG CAT GGT	484
Lys Leu Val Pro Trp Ser Gln Cys Arg Lys Asn Phe Leu Leu His Gly	
60 65 70	
TCC AAA AAT CTT ACC AAT TCA AGC TGT CTA AAA TTG GCA AGA CAA AAC	532
Ser Lys Asn Val Thr Asn Ser Ser Cys Leu Lys Leu Ala Arg Gln Asn	
75 80 85 90	
ACT AAT GGT CGT CAG AAA AAC AAG CCT CCT GAG CAC GTT ATA GAC TGT	580
Ser Asn Gly Gly Gln Lys Asn Lys Pro Pro Glu His Val Ile Asp Cys	
95 100 105	
GGA GAC ATA GTC TGG AGT CTT GCT TTT GGG TCT TCA GTT CCA GAA AAA	628
Gly Asp Ile Val Trp Ser Leu Ala Phe Gly Ser Ser Val Pro Glu Lys	
110 115 120	
CAG AGT CGT TGC GTT AAT ATA GAA TGG CAT CGG TTC CGA TTT GGA CAG	676
Gln Ser Arg Cys Val Asn Ile Glu Trp His Arg Phe Arg Phe Gly Gln	
125 130 135	
GAT CAG CTA CTC CTT GCC ACA GGA TTA AAC AAT GGT CGC ATC AAA ATC	724
Asp Gln Leu Leu Leu Ala Thr Gly Leu Asn Asn Gly Arg Ile Lys Ile	
140 145 150	
TGG GAT GTA TAT ACA GGA AAA CTC CTC CTT AAT TTG GTA GAC CAC ATT	772
Trp Asp Val Tyr Thr Gly Lys Leu Leu Leu Asn Leu Val Asp His Ile	
155 160 165 170	
GAA ATG GTT AGA GAT TTA ACT TTT GCT CCA GAT GGG AGC TTA CTC CTT	820
Glu Met Val Arg Asp Leu Thr Phe Ala Pro Asp Gly Ser Leu Leu Leu	
175 180 185	
GTA TCA GCT TCA AGA GAC AAA ACT CTA AGA GTG TGG GAC CTG AAA GAT	868
Val Ser Ala Ser Arg Asp Lys Thr Leu Arg Val Trp Asp Leu Lys Asp	
190 195 200	
GAT GGA AAC ATG GTG AAA GTA TTG CGG GCA CAT CAG AAT TGG GTG TAC	916
Asp Gly Asn Met Val Lys Val Leu Arg Ala His Gln Asn Trp Val Tyr	
205 210 215	
ACT TGT GCA TTC TCT CCC GAC TGT TCT ATG CTG TGT TCA GTG GGC GCC	964

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Ser Cys Ala Phe Ser Pro Asp Cys Ser Met Leu Cys Ser Val Gly Ala	
220 225 230	
AGT AAA GCA GTT TTC CTT TGG AAT ATG GAT AAA TAC ACC ATG ATT AGG	1012
Ser Lys Ala Val Phe Leu Trp Asn Met Asp Lys Tyr Thr Met Ile Arg	
235 240 245 250	
AAG CTG GAA GGT CAT CAC CAT GAT GTT GTA GCT TGT GAC TTT TCT CCT	1060
Lys Leu Glu Gly His His His Asp Val Val Ala Cys Asp Phe Ser Pro	
255 260 265	
GAT GGA GCA TTG CTA GCT ACT GCA TCC TAT GAC ACT CGT GTG TAT GTC	1108
Asp Gly Ala Leu Leu Ala Thr Ala Ser Tyr Asp Thr Arg Val Tyr Val	
270 275 280	
TGG GAT CCA CAC AAT GGA GAC CTT CTG ATG GAG TTT GGG CAC CTG TTT	1156
Trp Asp Pro His Asn Gly Asp Leu Leu Met Glu Phe Gly His Leu Phe	
285 290 295	
CCC TCG CCC ACT CCA ATA TTT GCT GGA GGA GCA AAT GAC CGA TGG GTG	1204
Pro Ser Pro Thr Pro Ile Phe Ala Gly Gly Ala Asn Asp Arg Trp Val	
300 305 310	
ACA GCT CTG TCT TTC AGT CAT GAT GGA CTG CAT GTT GCC AGC CTT GCT	1252
Arg Ala Val Ser Phe Ser His Asp Gly Leu His Val Ala Ser Leu Ala	
315 320 325 330	
GAT GAT AAA ATG CTG AGC TTC TGG AGA ATC GAT GAG GAT TGT CCG GTA	1300
Asp Asp Lys Met Val Arg Phe Trp Arg Ile Asp Glu Asp Cys Pro Val	
335 340 345	
CAA GTT GCA CCT TTG AGC AAT GGT CTT TGC TGT GCC TTT TCT ACT GAT	1348
Gln Val Ala Pro Leu Ser Asn Gly Leu Cys Cys Ala Phe Ser Thr Asp	
350 355 360	
GCC AGT GTT TTA GCT GCT GGG ACA CAT GAT GGA AGT GTG TAT TTT TGG	1396
Gly Ser Val Leu Ala Ala Gly Thr His Asp Gly Ser Val Tyr Phe Trp	
365 370 375	
GCC ACT CCA AGG CAA GTC CCT AGC CTT CAA CAT ATA TGT CGC ATG TCA	1444
Ala Thr Pro Arg Gln Val Pro Ser Leu Gln His Ile Cys Arg Met Ser	
380 385 390	
ATC CGA AGA GTG ATG TCC ACC CAA GAA GTC CAA AAA CTG CCT GTT CCT	1492
Ile Arg Arg Val Met Ser Thr Gln Glu Val Gln Lys Leu Pro Val Pro	



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395	400	405	410	
TCC AAA ATA TTG GCG TTT CTC TCC TAC CGC GGT TAG A CTGAAGACTG				1539
Ser Lys Ile Leu Ala Phe Leu Ser Tyr Arg Gly *				
	415	420		
CCTTTCTCTGG TAGGCCTGCC AGACAGAGCG CCCTTTACAA GACACACCTC AAGCTTTACC				1599
TCGTGCCGAA TT				1611

## (2) INFORMATION FOR SEQ ID NO:14:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 422 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met	Ala	Ser	Phe	Pro	Pro	Arg	Val	Asn	Glu	Lys	Glu	Ile	Val	Arg	Ser
1				5				10						15	
Arg	Thr	Ile	Gly	Glu	Leu	Leu	Ala	Pro	Ala	Ala	Pro	Phe	Asp	Lys	Lys
			20				25						30		
Cys	Gly	Gly	Glu	Asn	Trp	Thr	Val	Ala	Phe	Ala	Pro	Asp	Gly	Ser	Tyr
	35					40						45			
Phe	Ala	Trp	Ser	Gln	Gly	Tyr	Arg	Ile	Val	Lys	Leu	Val	Pro	Trp	Ser
	50					55					60				
Gln	Cys	Arg	Lys	Asn	Phe	Leu	Leu	His	Gly	Ser	Lys	Asn	Val	Thr	Asn
65				70					75					80	
Ser	Ser	Cys	Leu	Lys	Leu	Ala	Arg	Gln	Asn	Ser	Asn	Gly	Gly	Gln	Lys
			85					90						95	
Asn	Lys	Pro	Pro	Gln	His	Val	Ile	Asp	Cys	Gly	Asp	Ile	Val	Trp	Ser
			100					105					110		
Leu	Ala	Phe	Gly	Ser	Ser	Val	Pro	Glu	Lys	Gln	Ser	Arg	Cys	Val	Asn
	115						120					125			

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Ile	Glu	Trp	His	Arg	Phe	Arg	Phe	Gly	Gln	Asp	Gln	Leu	Leu	Leu	Ala
130							135					140			
Thr	Gly	Leu	Asn	Asn	Gly	Arg	Ile	Lys	Ile	Trp	Asp	Val	Tyr	Thr	Gly
145					150					155					160
Lys	Leu	Leu	Leu	Asn	Leu	Val	Asp	His	Ile	Glu	Met	Val	Arg	Asp	Leu
				165					170					175	
Thr	Phe	Ala	Pro	Asp	Gly	Ser	Leu	Leu	Leu	Val	Ser	Ala	Ser	Arg	Asp
			180						185					190	
Lys	Thr	Leu	Arg	Val	Trp	Asp	Leu	Lys	Asp	Asp	Gly	Asn	Met	Val	Lys
		195					200					205			
Val	Leu	Arg	Ala	His	Gln	Asn	Trp	Val	Tyr	Ser	Cys	Ala	Phe	Ser	Pro
210						215						220			
Asp	Cys	Ser	Met	Leu	Cys	Ser	Val	Gly	Ala	Ser	Lys	Ala	Val	Phe	Leu
225					230					235					240
Trp	Asn	Met	Asp	Lys	Tyr	Thr	Met	Ile	Arg	Lys	Leu	Glu	Gly	His	His
				245					250					255	
His	Asp	Val	Val	Ala	Cys	Asp	Phe	Ser	Pro	Asp	Gly	Ala	Leu	Leu	Ala
			260					265						270	
Thr	Ala	Ser	Tyr	Asp	Thr	Arg	Val	Tyr	Val	Trp	Asp	Pro	His	Asn	Gly
		275					280					285			
Asp	Leu	Leu	Met	Glu	Phe	Gly	His	Leu	Phe	Pro	Ser	Pro	Thr	Pro	Ile
290						295						300			
Phe	Ala	Gly	Gly	Ala	Asn	Asp	Arg	Trp	Val	Arg	Ala	Val	Ser	Phe	Ser
305					310					315					320
His	Asp	Gly	Leu	His	Val	Ala	Ser	Leu	Ala	Asp	Asp	Lys	Met	Val	Arg
			325						330					335	
Phe	Trp	Arg	Ile	Asp	Glu	Asp	Cys	Pro	Val	Gln	Val	Ala	Pro	Leu	Ser
		340						345					350		
Asn	Gly	Leu	Cys	Cys	Ala	Phe	Ser	Thr	Asp	Gly	Ser	Val	Leu	Ala	Ala
		355					360						365		

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Gly Thr His Asp Gly Ser Val Tyr Phe Trp Ala Thr Pro Arg Gln Val  
 370 375 380

Pro Ser Leu Gln His Ile Cys Arg Met Ser Ile Arg Arg Val Met Ser  
 385 390 395 400

Thr Gln Glu Val Gln Lys Leu Pro Val Pro Ser Lys Ile Leu Ala Phe  
 405 410 415

Leu Ser Tyr Arg Gly \*  
 420

## (2) INFORMATION FOR SEQ ID NO:15:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 783 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CTGTCTTCCT CCGCAGCGCG AGGCTGGGTA CAGGCTCTAT TGTCTGTGGT TGACTCCGTA	60
CTTTGGTCTG AGGCCTTCGG GAGCTTTCCC GAGGCAGTTA GCAGAAGCCG CAGCGACCGC	120
CCCCGCCCCG CTCCTCTGTC CCTGGGCCCC GGAGACAAAC TTGGCGTCAC GCCCTCAGCG	180
GTCGCCACTC TCTTCTCTGT TGTGGGTCC GCATCGTATT CCCGGAATCA GACGGTGCCC	240
CATAGATGGC CAGCTTTCCC CCGAGGGTCA ACGAGAAAGA GATCGTGAGA TCACGTACTA	300
TAGGTGAAC TTTAGCTCCT GCAGCTCCTT TTGACAAGAA ATGTGGTCGT GAAAATTGGA	360
CTGTTGCTTT TGCTCCAGAT GGTTCATACT TTGCTTGGTC ACAAGGACAT CGCACAGTAA	420
AGCTTGTTCC GTGGTCCCAG TGCTTCAGA ACTTTCTCTT GCATGGCACC AAGAATGTTA	480
OCAATTCAAG CAGTTTAAGA TTGCCAAGAC AAAATAGTGA TGGTGGTCAG AAAAATAAGC	540
CTCGTGACAT ATTATAGACT GTGGAGATAT AGTCTGGAGT CTTGCTTTTG GGTCAACAGT	600

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TCCAGAAAAA CAGAGTCGCT GTGTAAATAT AGAATGGCAT CGCTTCAGAT TTGGACAAGA 660  
 TCAGCTACTT CTGCTACAG GGTGAACAA TGGGCGTATC AAAATATGGG ATGTATATCA 720  
 GGAAACTCCT CCTTAAGTGT GTAGATCATA CTGAAGTGGT CAGAGATTTA ACTTTTGCTC 780  
 CAG 783

## (2) INFORMATION FOR SEQ ID NO:16:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1122 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CTCTGTATGT CTGAATGAAG CTATAACATT TGCCTTTTTTA TTGCAGGTTT TCCTTTGGAA 60  
 TATGGATAAA TACACCATGA TACGGAAACT AGAAGGACAT CACCATGATG TGCTAGCTTG 120  
 TGACTTTTCT CCTGATGGAG CATTACTGGC TACTGCATCT TATGATACTC GAGTATATAT 180  
 CTGGGATCCA CATAATGGAG ACATTCTGAT GGAATTTGGG CACCTGTTTC CCCACCTAC 240  
 TCCAATATTT GCTGGAGGAG CAAATGACCG GTGGGTACGA TCTGTATCTT TTAGCCATGA 300  
 TGGACTGCAT GTTGCAAGCC TTGCTGATGA TAAAATGGTG AGGTTCTGGA GAATPGATGA 360  
 GGATTATCCA GTGCAAGTTG CACCTTTGAG CAATGGTCTT TGCTGTGCCT TCTCTACTGA 420  
 TGGCAGTGT TTAGCTGCTG GGACACATGA CGGAAGTGTG TATTTTTGGG CCACTCCACG 480  
 GCAGGTCCCT AGCCTGCAAC ATTTATGTCG CATGTCAATC CGAAGAGTGA TCCCCACCCA 540  
 AGAAGTTCAG GAGCTGCCGA TTCCTTCCAA GCTTTTGGAG TTTCTCTCGT ATCGTATTTA 600  
 GAAGATTCTG CCTTCCCTAG TAGTAGGGAC TGACAGAATA CACTTAACAC AAACCTCAAG 660  
 CTTTACTGAC TTCAATTATC TGTFTTTAAA GACGTAGAAG ATTTATTTAA TTTGATATGT 720

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TCTTGACTG CATTGATC AGTTGAGCTT TTAAATATT ATTTATAGAC AATAGAAGTA      780
TTTCTGAACA TATCAAATAT AAATTTTTTT AAAGATCTAA CTGTGAAAAC ATACATACCT      840
GTACATATTT AGATATAAGC TGCTATATGT TGAATGGACC CTTTTCCTTT TCTGATTTTT      900
AGTTCTGACA TGTATAEATT GCTTCAGTAG AGCCACAATA TGTATCTTTG CTGTAAAGTG      960
CAAGGAAATT TTAAATTCTG GGACACTGAG TTAGATGGTA AATFACTGACT TACGAAAGTT     1020
GAATTCGGTG AGCCCGCCAA ATCACTGAG GTCAGCAGTT TGAGACTAGC CTGGCAAACA     1080
TGATGAAACC CTGTCTCTAC TAAAAATACA AAAAAAAAAA AA                        1122

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## (2) INFORMATION FOR SEQ ID NO:17:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2537 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 422..2029

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

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CGGCACGAGC CGGGCTCCGT CCGGAGGAAG CGAGGCTGCG CCGCCGGCCC GCCAGGAGCG      60
GAGGACGGGA GCGCGGGCGG TCGCGCTCGC CCTGTCGCTG ACTGCGCTGC CCCGCCCCAT      120
CCTTGCTTGG CCGCAGGTGC CCTGGATGAG GCGCGCGCGC GTGTCCCGGC CCTGAGTGT      180
CCCCCGGGGT CGCCCGGCGC CTGCCCTCAA GCGGCCGCCCT CTCCTTGCCC GGGTCCCCGT      240
TTTCCCCCGG CGCAGTCCTC CTCGGGTGGG CCGCTCCGCA CCTCGGCGCA GCGGACCGG      300
CCTTCGGGCC GGGATGGATC CGCCGGGAAG AGGAAGACAA GCGGGGGCGT TGAGCCCCCTG      360

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CGCACGGTGC CGCCGCGCGT AGTGGGAGCT TACTCGCAGT AGGCTCTCGC TCTTCTAATC 420

A ATG GAT AAA GTG GGG AAA ATG TGG AAC AAC TTA AAA TAC AGA TGC 466  
Met Asp Lys Val Gly Lys Met Trp Asn Asn Leu Lys Tyr Arg Cys  
1 5 10 15

CAG AAT CTC TTC AGC CAC GAG GGA GGA AGC CGT AAT GAG AAC GTG GAG 514  
Gln Asn Leu Phe Ser His Glu Gly Gly Ser Arg Asn Glu Asn Val Glu  
20 25 30

ATG AAC CCC AAC AGA TGT CCG TCT GTC AAA GAG AAA AGC ATC AGT CTG 562  
Met Asn Pro Asn Arg Cys Pro Ser Val Lys Glu Lys Ser Ile Ser Leu  
35 40 45

GGA GAG GCA GCT CCC CAG CAA GAG AGC AGT CCC TTA AGA GAA AAT GTT 610  
Gly Glu Ala Ala Pro Gln Gln Glu Ser Ser Pro Leu Arg Glu Asn Val  
50 55 60

GCC TTA CAG CTG GGA CTG AGC CCT TCC AAG ACC TTT TCC AGC CGG AAC 658  
Ala Leu Gln Leu Gly Leu Ser Pro Ser Lys Thr Phe Ser Arg Arg Asn  
65 70 75

CAA AAC TGT GCC GCA GAG ATC CCT CAA GTG GTT GAA ATC AGC ATC GAG 706  
Gln Asn Cys Ala Ala Glu Ile Pro Gln Val Val Glu Ile Ser Ile Glu  
80 85 90 95

AAA GAC AGT GAC TCG GGT GCC ACC CCA GGA ACG AGG CTT GCA CGG AGA 754  
Lys Asp Ser Asp Ser Gly Ala Thr Pro Gly Thr Arg Leu Ala Arg Arg  
100 105 110

GAC TCC TAC TCG CGG CAC GCC CCG TGG GGA GGA AAG AAG AAA CAT TCC 802  
Asp Ser Tyr Ser Arg His Ala Pro Trp Gly Gly Lys Lys Lys His Ser  
115 120 125

TGT TCC ACA AAG ACC CAG AGT TCA TTG GAT ACC GAG AAA AAG TTT GGT 850  
Cys Ser Thr Lys Thr Gln Ser Ser Leu Asp Thr Glu Lys Lys Phe Gly  
130 135 140

AGA ACT CGA AGC GCC CTT CAG AGG CGA GAG CGG CGC TAT GGA GTC AGC 898  
Arg Thr Arg Ser Gly Leu Gln Arg Arg Glu Arg Arg Tyr Gly Val Ser  
145 150 155

TCC ATG CAG GAC ATG GAC AGC GTT TCT AGC CGC GCG GTC GGG AGC CGC 946  
Ser Met Gln Asp Met Asp Ser Val Ser Ser Arg Ala Val Gly Ser Arg  
160 165 170 175

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TCC CTG AGG CAG AGG CTC CAG GAC ACG GTG GGT TPG TGT TTT CCC ATG	994
Ser Leu Arg Gln Arg Leu Gln Asp Thr Val Gly Leu Cys Phe Pro Met	
180 185 190	
AGA ACT TAC AGC AAG CAG TCA AAG CCA CTC TTT TCC AAT AAA AGA AAA	1042
Arg Thr Tyr Ser Lys Gln Ser Lys Pro Leu Phe Ser Asn Lys Arg Lys	
195 200 205	
ATA CAT CTT TCT GAA TTA ATG CTG GAG AAA TGC CCT TTT CCT GCT GGC	1090
Ile His Leu Ser Glu Leu Met Leu Glu Lys Cys Pro Phe Pro Ala Gly	
210 215 220	
TCG GAT TTA GCA CAA AAG TGG CAT TTG ATT AAA CAG CAT ACC GCC CCT	1138
Ser Asp Leu Ala Gln Lys Trp His Leu Ile Lys Gln His Thr Ala Pro	
225 230 235	
GTG AGC CCA CAC TCA ACA TTT TTT GAT ACA TTT GAT CCA TCA CTG GTG	1186
Val Ser Pro His Ser Thr Phe Phe Asp Thr Phe Asp Pro Ser Leu Val	
240 245 250 255	
TCT ACA GAA GAT GAA GAA GAT AGG CTT CGC GAG AGA AGA CGG CTT AGT	1234
Ser Thr Glu Asp Glu Glu Asp Arg Leu Arg Glu Arg Arg Arg Leu Ser	
260 265 270	
ATC GAA GAA GGG GTG GAT CCC CCT CCC AAC GCA CAA ATA CAC ACC TTT	1282
Ile Glu Glu Gly Val Asp Pro Pro Pro Asn Ala Gln Ile His Thr Phe	
275 280 285	
GAA GCT ACT GCA CAG GTC AAC CCA TTG TAT AAG CTG GGA CCA AAG TTA	1330
Glu Ala Thr Ala Gln Val Asn Pro Leu Tyr Lys Leu Gly Pro Lys Leu	
290 295 300	
GCT CCT GGG ATG ACA GAG ATA AGT GGA GAT GGT TCT GCA ATT CCA CAA	1378
Ala Pro Gly Met Thr Glu Ile Ser Gly Asp Gly Ser Ala Ile Pro Gln	
305 310 315	
GCA ATT GTG ACT CAG AAG AGG ATT CAA CCA CCC TAT GTC TGC AGT CAC	1426
Ala Ile Val Thr Gln Lys Arg Ile Gln Pro Pro Tyr Val Cys Ser His	
320 325 330 335	
GGA GGC AGA AGC AGC GCC AGG TGT CCG GGG ACA GCC ACG CGC ACG TTA	1474
Gly Gly Arg Ser Ser Ala Arg Cys Pro Gly Thr Ala Thr Arg Thr Leu	
340 345 350	
GCA GAC AGG GAG CTT GGA AAG TTC ATA CGC AGA TCG ATT ACA TAC ACT	1522

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Ala Asp Arg Glu Leu Gly Lys Phe Ile Arg Arg Ser Ile Thr Tyr Thr	
355 360 365	
GCC TCG TGC CAG ATT TGC TTC AGA TCA CAG GGA ATC CCT GTT ACT GGG	1570
Ala Ser Cys Gln Ile Cys Phe Arg Ser Gln Gly Ile Pro Val Thr Gly	
370 375 380	
GCG TGA TGG ACC GAT ACG AGG CCG AAG CCC TTC TAG AAG GGA AAC CGG	1618
Ala * Trp Thr Asp Thr Arg Pro Lys Pro Phe * Lys Gly Asn Arg	
385 390 395	
AAG GCA CGT TCT TGC TCA GGG ACT CTG CAC AGG AGG ACT ACC TCT TCT	1666
Lys Ala Arg Ser Cys Ser Gly Thr Leu His Arg Arg Thr Thr Ser Ser	
400 405 410 415	
CTG TGA GCT TCC GCC GCT ACA ACA GGT CTC TGC ACG CCC GGA TCG AGC	1714
Leu * Ala Ser Ala Ala Thr Thr Gly Leu Cys Thr Pro Gly Ser Ser	
420 425 430	
AGT GGA ACC ACA ACT TCA GCT TCG ATG CCC ATG ACC CCT GCG TGT TTC	1762
Ser Gly Thr Thr Thr Ser Ala Ser Met Pro Met Thr Pro Ala Cys Phe	
435 440 445	
ACT CCT CCA CGT CAC GGG GCT TCT CGA ACA CTA TAA AGA CCC CAG CTC	1810
Thr Pro Pro Arg His Gly Ala Ser Arg Thr Leu * Arg Pro Gln Leu	
450 455 460	
TTG CAT GTT TTT TGA ACC GTT GCT AAC GAT ATC ACT GAA TAG AAC TTT	1858
Leu His Val Phe * Thr Val Ala Asn Asp Ile Thr Glu * Asn Phe	
465 470 475	
CCC TTT CAG CCT GCA GTA TAT CTG CCG CGC AGT GAT CTG CAG ATG CAC	1906
Pro Phe Gln Pro Ala Val Tyr Leu Pro Arg Ser Asp Leu Gln Met His	
480 485 490 495	
TAC GTA TGA TGG GAT TGA CCG GCT CCC GCT ACC GTC GAT GTT ACA GGA	1954
Tyr Val * Trp Asp * Arg Ala Pro Ala Thr Val Asp Val Thr Gly	
500 505 510	
TTT TTT AAA AGA GTA TCA TTA TAA ACA AAA AGT TAG GGT TCG CTG GTT	2002
Phe Phe Lys Arg Val Ser Leu * Thr Lys Ser * Gly Ser Leu Val	
515 520 525	
AGA ACG AGA CCA GTC AAA GCA AAG TAACCTCCTCT CCCCAGGG CACTAACTAA	2056
Arg Thr Arg Pro Val Lys Ala Lys	



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530	535	
GTCTGCTCCT CCCGTGCATC GAACTGCAAC CATAGGAGGC AGTCAGCTGC TAGGATTTCC	2116	
CACCCAGAAT GGGAGCTTAG TCATTAGCCT CTGCCCTATG GGGTCCGCTG TTCCTCAGAC	2176	
AAAGGTGCCT AGGGACAGCA AGATGGCTTG CAGGTGTTCC GTGGGCTGTG ACAACTGAGG	2236	
GAGGCAACTC TGGGGCATTG GCTATGAAGA ATTCTATTTC TTACCGAAGA ACAAATTATT	2296	
AATATTCGAT GGGTATTTCA ATAGTGTGAC TAATGTTTGA AATTATTTTT TCTAAGAATT	2356	
TTTCTATAAC CTTCAGAAAA AGTAGTGATG TTTGTAGTTA CTATAAATCA AGCTTTGAAA	2416	
GTTCAAAACA AACAAGTTAA ATAAAAGACT ACCTTCCTTT TAGAGAAAAC AAATGCAAGT	2476	
TTTCCCAGCC ACAGGCATTG TGCACGTGTA ATGTTGCTTG TTATCAGCTC CTTTCCTCTC	2536	
C	2537	

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 535 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Met	Asp	Lys	Val	Gly	Lys	Met	Trp	Asn	Asn	Leu	Lys	Tyr	Arg	Cys	Gln
1				5				10						15	
Asn	Leu	Phe	Ser	His	Glu	Gly	Gly	Ser	Arg	Asn	Glu	Asn	Val	Glu	Met
			20					25					30		
Asn	Pro	Asn	Arg	Cys	Pro	Ser	Val	Lys	Glu	Lys	Ser	Ile	Ser	Leu	Gly
			35					40					45		
Glu	Ala	Ala	Pro	Gln	Gln	Glu	Ser	Ser	Pro	Leu	Arg	Glu	Asn	Val	Ala
			50					55					60		
Leu	Gln	Leu	Gly	Leu	Ser	Pro	Ser	Lys	Thr	Phe	Ser	Arg	Arg	Asn	Gln

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65		70		75		80
Asn Cys Ala Ala Glu Ile Pro Gln Val Val Glu Ile Ser Ile Glu Lys						
	85		90			95
Asp Ser Asp Ser Gly Ala Thr Pro Gly Thr Arg Leu Ala Arg Arg Asp						
	100		105			110
Ser Tyr Ser Arg His Ala Pro Trp Gly Gly Lys Lys Lys His Ser Cys						
	115		120			125
Ser Thr Lys Thr Gln Ser Ser Leu Asp Thr Glu Lys Lys Phe Gly Arg						
	130		135			140
Thr Arg Ser Gly Leu Gln Arg Arg Glu Arg Arg Tyr Gly Val Ser Ser						
	145		150			155
Met Gln Asp Met Asp Ser Val Ser Ser Arg Ala Val Gly Ser Arg Ser						
		165		170		175
Leu Arg Gln Arg Leu Gln Asp Thr Val Gly Leu Cys Phe Pro Met Arg						
	180		185			190
Thr Tyr Ser Lys Gln Ser Lys Pro Leu Phe Ser Asn Lys Arg Lys Ile						
	195		200			205
His Leu Ser Glu Leu Met Leu Glu Lys Cys Pro Phe Pro Ala Gly Ser						
	210		215			220
Asp Leu Ala Gln Lys Trp His Leu Ile Lys Gln His Thr Ala Pro Val						
	225		230			235
Ser Pro His Ser Thr Phe Phe Asp Thr Phe Asp Pro Ser Leu Val Ser						
		245		250		255
Thr Glu Asp Glu Glu Asp Arg Leu Arg Glu Arg Arg Arg Leu Ser Ile						
	260		265			270
Glu Glu Gly Val Asp Pro Pro Pro Asn Ala Gln Ile His Thr Phe Glu						
	275		280			285
Ala Thr Ala Gln Val Asn Pro Leu Tyr Lys Leu Gly Pro Lys Leu Ala						
	290		295			300
Pro Gly Met Thr Glu Ile Ser Gly Asp Gly Ser Ala Ile Pro Gln Ala						

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305                      310                      315                      320  
 Ile Val Thr Gln Lys Arg Ile Gln Pro Pro Tyr Val Cys Ser His Gly  
                          325                      330                      335  
 Gly Arg Ser Ser Ala Arg Cys Pro Gly Thr Ala Thr Arg Thr Leu Ala  
                          340                      345                      350  
 Asp Arg Gln Leu Gly Lys Phe Ile Arg Arg Ser Ile Thr Tyr Thr Ala  
                          355                      360                      365  
 Ser Cys Gln Ile Cys Phe Arg Ser Gln Gly Ile Pro Val Thr Gly Ala  
                          370                      375                      380  
 \* Trp Thr Asp Thr Arg Pro Lys Pro Phe \* Lys Gly Asn Arg Lys  
 385                      390                      395                      400  
 Ala Arg Ser Cys Ser Gly Thr Leu His Arg Arg Thr Thr Ser Ser Leu  
                          405                      410                      415  
 \* Ala Ser Ala Ala Thr Thr Gly Leu Cys Thr Pro Gly Ser Ser Ser  
                          420                      425                      430  
 Gly Thr Thr Thr Ser Ala Ser Met Pro Met Thr Pro Ala Cys Phe Thr  
                          435                      440                      445  
 Pro Pro Arg His Gly Ala Ser Arg Thr Leu \* Arg Pro Gln Leu Leu  
                          450                      455                      460  
 His Val Phe \* Thr Val Ala Asn Asp Ile Thr Glu \* Asn Phe Pro  
 465                      470                      475                      480  
 Phe Gln Pro Ala Val Tyr Leu Pro Arg Ser Asp Leu Gln Met His Tyr  
                          485                      490                      495  
 Val \* Trp Asp \* Arg Ala Pro Ala Thr Val Asp Val Thr Gly Phe  
                          500                      505                      510  
 Phe Lys Arg Val Ser Leu \* Thr Lys Ser \* Gly Ser Leu Val Arg  
                          515                      520                      525  
 Thr Arg Pro Val Lys Ala Lys  
                          530                      535

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## (2) INFORMATION FOR SEQ ID NO:19:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1221 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

```

GATTAAACAG CATACAGCTC CTGTGAGCCC ACAATCAACA TTTTGTGATA CTTTGATCCA      60
TCTTTGGTTT CTACAGAAGA TGAAGAAGAT AGGCTTAGAG AGAGAAGGCG GCTTAGTATT      120
GAAGAAGGGG TTGATCCCCC TCCCAATGCA CAAATACATA CATTGGAAGC TACTGCACAG      180
GTAAATCCAT TATTAAACTG GGACCAAAAT TAGCTCCTGG AATGACTGAA ATAAGTGGGG      240
ACAGTTCTGC AATCCACAA GCTAATTGTG ACTCGGAAGA GGATACAACC ACCCTGTGTT      300
GCAGTCACGG AGGCAGAAGC AGCGTCAGAT ATCTGGAGAC AGCCATACCC ATGTTAGCAG      360
ACAGGGAGCT TGGAAAGTCC ACACACAGAT TGATTACATA CACTGCTTCG TGCCTGATTT      420
GCTTCAAATT ACAGGGAATC CCTGTTACTG GGGAGTGATG GACCGTTATG AAGCAGAAGC      480
CCTTCTCGAA GGGAAACCTG AAGGCACGTT TTTGCTCAGG GACTCTGGCG AAGAGGACTA      540
CTTCTTCTCT GTGAGCTTCC GCCGATACAA CAGATCCCTG CATGCCCCGA TTGAGCAGTG      600
GAATCACAAC TTTAGTTTCG ACGCCATGA CCCGTGTGTA TTCACTCCT CCACTGTAAC      660
GGGACTTTTA GAACATTATA AAGATCCCAG TTCGTGCATG TTTTGTGAAC CATTGCTTAC      720
TATATCACTA AATAGGACTT TCCCTTTTAG CCTGCAGTAT ATCTGTGCGG CGGTAATCTG      780
CAGGTGCACT ACGTATGATG GAATTGATGG GCTCCCTCTA CCCTCAATGT TACAGGATTT      840
TTTAAAAGAG TATCATTATA AACAAAAAGT TAGAGTTGCG TGGTTGGAAC GAGAACCAGT      900
CAAGGCAAAG TAAACTCTCC GGTCCCCAAA GGGTGTTAAC TAGGTCCGCT TTCATGTGCA      960

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TCAGACAGTA CACCTATAGC AAGCACACGT AGCAGTGTTA GGCTTTTTC A TACAGTATGT 1020
AAGCTTAGTG TTAGTATCTG TCAGATGCTA CCGCTGTGTA CTTATTCAGA TAAACATGGT 1080
GCCTATTGGA ACAATAGCGG ATAGAGCTAC AGGTGTTTCA TAAGACTACA AAAACATTTT 1140
GCCTATTTTG CTAACAGTTT GGTFTTTTAA GGCTGTGGTA TTTGAGTGAG GCAACTCTGG 1200
GCCATTTGTT ATGAAGAAAT G 1221

```

## (2) INFORMATION FOR SEQ ID NO:20:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2369 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 116..1330

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

```

GGCACCAGGC SGTGGTGGCG GCGGCGGGCG CGGCCGCGGC GGGGCGGGCG CGGAATGAAG 60
GGCCACGGCC CTGGGGGCTG AGGCGCCCGC CGCCTGGGGC GGGCCGCGCG TCCTC ATG 118
Met
1
GAG GCC GGA GAG GAG CCG CTG CTG CTG GCT GAA CTC AAG CCT GGG CGC 166
Glu Ala Gly Glu Glu Pro Leu Leu Leu Ala Glu Leu Lys Pro Gly Arg
5 10 15
CCC CAC CAG TTC GAC TGG AAG TCA AGC TGC GAG ACC TGG AGC GTG GCC 214
Pro His Gln Phe Asp Trp Lys Ser Ser Cys Glu Thr Trp Ser Val Ala
20 25 30
TTC TCG CCA GAC GGT TCC TGG TTC GCC TGG TCT CAA GGA CAC TGC GTG 262

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Phe Ser Pro Asp Gly Ser Trp Phe Ala Trp Ser Gln Gly His Cys Val	
35 40 45	
GTC AAG CTG GTC CCC TGG CCC TTA GAG GAA CAG TTC ATC CCT AAA GGA	310
Val Lys Leu Val Pro Trp Pro Leu Glu Glu Gln Phe Ile Pro Lys Gly	
50 55 60 65	
TTC GAA GCC AAG AGC CGA AOC AGC AAG AAT GAC CCA AAA GGA CGG GGC	358
Phe Glu Ala Lys Ser Arg Ser Ser Lys Asn Asp Pro Lys Gly Arg Gly	
70 75 80	
AGT CTG AAG GAG AAG ACG CTG GAC TGT GGC CAG ATT GTG TGG GGG CTG	406
Ser Leu Lys Glu Lys Thr Leu Asp Cys Gly Gln Ile Val Trp Gly Leu	
85 90 95	
GCC TTC AGC CCG TGG CCC TCT CCA CCC AGC AGG AAA CTC TGG GCA CCT	454
Ala Phe Ser Pro Trp Pro Ser Pro Pro Ser Arg Lys Leu Trp Ala Arg	
100 105 110	
CAC CAT CCC CAG GCG CCT GAT GTT TCT TGC CTG ATC CTG GCC ACA GGT	502
His His Pro Gln Ala Pro Asp Val Ser Cys Leu Ile Leu Ala Thr Gly	
115 120 125	
CTC AAC GAT GGG CAG ATC AAG ATT TGG GAG GTA CAG ACA GGC CTC CTG	550
Leu Asn Asp Gly Gln Ile Lys Ile Trp Glu Val Gln Thr Gly Leu Leu	
130 135 140 145	
CTT CTG AAT CTT TCT GGC CAC CAA GAC GTC GTG AGA GAT CTG AGC TTC	598
Leu Leu Asn Leu Ser Gly His Gln Asp Val Val Arg Asp Leu Ser Phe	
150 155 160	
ACG CCC AGC GGC AGT TTG ATT TTG CTC TCT GCA TCC CGG GAT AAG ACA	646
Thr Pro Ser Gly Ser Leu Ile Leu Val Ser Ala Ser Arg Asp Lys Thr	
165 170 175	
CTT CGA ATT TGG GAC CTG AAT AAA CAC GGT AAG CAG ATC CAG GTG TTA	694
Leu Arg Ile Trp Asp Leu Asn Lys His Gly Lys Gln Ile Gln Val Leu	
180 185 190	
TCC GGC CAT CTG CAG TGG GTT TAC TGC TGC TCC ATC TCC CCT GAC TGT	742
Ser Gly His Leu Gln Trp Val Tyr Cys Cys Ser Ile Ser Pro Asp Cys	
195 200 205	
AGC ATG CTG TGC TCT GCA GCT GGG GAG AAG TCG GTC TTT CTG TGG AGC	790
Ser Met Leu Cys Ser Ala Ala Gly Glu Lys Ser Val Phe Leu Trp Ser	

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210	215	220	225	
ATG CGG TCC TAC ACA CTA ATC CGG AAA CTA GAA GGC CAC CAA AGC AGT				838
Met Arg Ser Tyr Thr Leu Ile Arg Lys Leu Glu Gly His Gln Ser Ser				
	230	235	240	
GTT GTC TCC TGT GAT TTC TCT CCT GAT TCA GCC TTG CTT GTC ACA GCT				886
Val Val Ser Cys Asp Phe Ser Pro Asp Ser Ala Leu Leu Val Thr Ala				
	245	250	255	
TCG TAT GAC ACC AGT GTG ATT ATG TGG GAC CCC TAC ACC GGC GCG AGG				934
Ser Tyr Asp Thr Ser Val Ile Met Trp Asp Pro Tyr Thr Gly Ala Arg				
	260	265	270	
CTG AGG TCA CTT CAT CAC ACA CAA CTT GAA CCC ACC ATG GAT GAC AGT				982
Leu Arg Ser Leu His His Thr Gln Leu Glu Pro Thr Met Asp Asp Ser				
	275	280	285	
GAC GTC CAC ATG AGC TCC CTG AGG TCC GTG TGC TTC TCA CCT GAA GGC				1030
Asp Val His Met Ser Ser Leu Arg Ser Val Cys Phe Ser Pro Glu Gly				
	290	295	300	305
TTG TAT CTC GCT ACG GTG GCA GAT GAC AGG CTG CTC AGG ATC TGG GCT				1078
Leu Tyr Leu Ala Thr Val Ala Asp Asp Arg Leu Leu Arg Ile Trp Ala				
	310	315	320	
CTG GAA CTG AAG GCT CCG GTT GCC TTT GCT CCG ATG ACC AAT GGT CTT				1126
Leu Glu Leu Lys Ala Pro Val Ala Phe Ala Pro Met Thr Asn Gly Leu				
	325	330	335	
TGC TGC ACG TTC TTC CCA CAC GGT GGA ATT ATT GCC ACA GGG ACG AGA				1174
Cys Cys Thr Phe Phe Pro His Gly Gly Ile Ile Ala Thr Gly Thr Arg				
	340	345	350	
GAT GGC CAT GTC CAG TTC TGG ACA GCT CCC CGG GTC CTG TCC TCA CTG				1222
Asp Gly His Val Gln Phe Trp Thr Ala Pro Arg Val Leu Ser Ser Leu				
	355	360	365	
AAG CAC TTA TGC AGG AAA GCC CTC CGA AGT TTC CTG ACA ACG TAT CAA				1270
Lys His Leu Cys Arg Lys Ala Leu Arg Ser Phe Leu Thr Thr Tyr Gln				
	370	375	380	385
GTC CTA GCA CTG CCA ATC CCC AAG AAG ATG AAA GAG TTC CTC ACA TAC				1318
Val Leu Ala Leu Pro Ile Pro Lys Lys Met Lys Glu Phe Leu Thr Tyr				
	390	395	400	

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AGG ACT TTC TAGCAGTGCC GGCTCCCCCA CCTCTGCAG CAGCAGCAGT	1367
Arg Thr Phe	
405	
ACAAGGGACT GGCTAGGATG GAGTCAGGCA GCTCACACTG GACCAGTGTG GACCTTCCTT	1427
CCTCCCATGG CATGTGCAAG TAGGTCTGCG TGACCCCACT TCTGTGGTGC CGGCCTTACC	1487
TCGTCTTCAT CCGTGGTGAG CAGCCTTCGT CAGTCTAGTT GTGTGAAGC CAAGTGCAGT	1547
TGTGGATGTT GCTGGGGTAA TAAAGGCAAG CGGGCTCCAG AGCCTCTCTG GTGGCGGCCA	1607
AGCCACACTC CCTTAACTGG GAAGTACCTG CCACGTAGGG CATTTCTGCT GCCTATTTCC	1667
AGCCAGCGGC TGCATGGTTT GAAGTTCCCTC CGTGTGGTC AGAAGAACTC TGGTGTTTGG	1727
TTCCCTGCTC AGCTGCGCGT GGACTGGGCT GAGCTCCTCA CCAATACATA GTGCCGGCTT	1787
TTGTTTCCTG TAAACAGTGG TTGCATGTGT AGAGAAGTAA CAAGCCAGTA TTCAGATCAT	1847
ACGAGGAGGC GTTCTCGGT GCATGACGGT CAGATGGCCA TTTATCAGCA TATTTATTTG	1907
TATTTTCTCA GCACATAGTA AGGTACAAC TGTGTTTCTC AATGTCTCG AAAAAACAGA	1967
GTTCCTAAGT GSCCCAGTTG TGGAGCCAAG TCTAAGTCGT GTGGAGTCAG TGCTGACATC	2027
ACTGGCTTGT GCTGTCTGTC ACATGTGTTT GTCTCTGCTG CTTGACCTCA TGGGATGTAC	2087
CCTCCAGTTC AACTGCCCAA AACAGACAGC CCCTTCCAAG CACCGTTCTT TGACACCGGT	2147
AGCAGCTACC TATTCAAGAC GCTCACACA AAATCTGCCT TAGAAAGTTA ATATATTTTA	2207
AATTATTTTA AAAGAACTC AACATCTTAT TCTTTGGCCT TTCTTAATTG ATGCTTTATG	2267
GAGGCAGTGT TAACATTGTA CAGTGTATGC ATAGAGGAGT CTCTCTATT TGAAGAACAA	2327
TGCAAAATGA GGCTTTCATT GAAGGGAAAA AAAAAAAAAA AA	2369

(2) INFORMATION FOR SEQ ID NO:21:

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 404 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

```

Met Glu Ala Gly Glu Glu Pro Leu Leu Leu Ala Glu Leu Lys Pro Gly
 1             5             10             15

Arg Pro His Gln Phe Asp Trp Lys Ser Ser Cys Glu Thr Trp Ser Val
          20             25             30

Ala Phe Ser Pro Asp Gly Ser Trp Phe Ala Trp Ser Gln Gly His Cys
          35             40             45

Val Val Lys Leu Val Pro Trp Pro Leu Glu Glu Gln Phe Ile Pro Lys
          50             55             60

Gly Phe Gln Ala Lys Ser Arg Ser Ser Lys Asn Asp Pro Lys Gly Arg
 65             70             75             80

Gly Ser Leu Lys Glu Lys Thr Leu Asp Cys Gly Gln Ile Val Trp Gly
          85             90             95

Leu Ala Phe Ser Pro Trp Pro Ser Pro Pro Ser Arg Lys Leu Trp Ala
          100            105            110

Arg His His Pro Gln Ala Pro Asp Val Ser Cys Leu Ile Leu Ala Thr
          115            120            125

Gly Leu Asn Asp Gly Gln Ile Lys Ile Trp Glu Val Gln Thr Gly Leu
          130            135            140

Leu Leu Leu Asn Leu Ser Gly His Gln Asp Val Val Arg Asp Leu Ser
          145            150            155            160

Phe Thr Pro Ser Gly Ser Leu Ile Leu Val Ser Ala Ser Arg Asp Lys
          165            170            175

Thr Leu Arg Ile Trp Asp Leu Asn Lys His Gly Lys Gln Ile Gln Val
          180            185            190

Leu Ser Gly His Leu Gln Trp Val Tyr Cys Cys Ser Ile Ser Pro Asp
          195            200            205

Cys Ser Met Leu Cys Ser Ala Ala Gly Glu Lys Ser Val Phe Leu Trp
          210            215            220

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Ser Met Arg Ser Tyr Thr Leu Ile Arg Lys Leu Glu Gly His Gln Ser			
225	230	235	240
Ser Val Val Ser Cys Asp Phe Ser Pro Asp Ser Ala Leu Leu Val Thr			
	245	250	255
Ala Ser Tyr Asp Thr Ser Val Ile Met Trp Asp Pro Tyr Thr Gly Ala			
	260	265	270
Arg Leu Arg Ser Leu His His Thr Gln Leu Glu Pro Thr Met Asp Asp			
	275	280	285
Ser Asp Val His Met Ser Ser Leu Arg Ser Val Cys Phe Ser Pro Glu			
	290	295	300
Gly Leu Tyr Leu Ala Thr Val Ala Asp Asp Arg Leu Leu Arg Ile Trp			
305	310	315	320
Ala Leu Glu Leu Lys Ala Pro Val Ala Phe Ala Pro Met Thr Asn Gly			
	325	330	335
Leu Cys Cys Thr Phe Phe Pro His Gly Gly Ile Ile Ala Thr Gly Thr			
	340	345	350
Arg Asp Gly His Val Gln Phe Trp Thr Ala Pro Arg Val Leu Ser Ser			
	355	360	365
Leu Lys His Leu Cys Arg Lys Ala Leu Arg Ser Phe Leu Thr Thr Tyr			
	370	375	380
Gln Val Leu Ala Leu Pro Ile Pro Lys Lys Met Lys Glu Phe Leu Thr			
385	390	395	400
Tyr Arg Thr Phe			

(2) INFORMATION FOR SEQ ID NO:22:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1246 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GACACTGCAT CGTCAAAC TG ATCCCC TGGC CGTTGGAGGA GCAGTTCATC CCTAAAGGGT	50
TTGAAGCCAA AAGCCGAAGT AGCAAAAATG AGACGAAAGG GCGGGGCAGC CCAAAAGAGA	120
AGACGCTGGA CTGTGGTCAG ATTGTCTGGG GGCTGSCCTT CAGCCTGTGC TTTCCCCACC	180
CAGCAGGAAG CTCTGGGCAC GCCACCACCC CCAAGTGCCC GATGTCTCTT GCCTGGTTCT	240
TGCTACGGGA CTCACGATG GGCAGATCAA GATCTGGGAG GTGCAGACAG GGCTCCTGCT	300
TTTGAATCTT TCCGGCCACC AAGATGTCTT GAGAGATCTG AGCTTCACAC CCAGTGGCAG	360
TTTGATTTG GTCTCCGCT CACGGGATAA GACTCTTGGC ATCTGGGACC TGAATAACA	420
CGGTAAACAG ATTCAAGTGT TATCGGGCCA CCTGCAGTGG GTTTACTGCT GTTCCATCTC	480
CCCAGACTGC AGCATGCTGT GCTCTGCAGC TGGAGAGAAG TCGGTCTTTC TATGGAGCAT	540
GAGGTCTTAC ACCTTAATTC GGAAGCTAGA GGGCCATCAA AGCAGTGTG TCTCTTGTGA	600
CTTCTCCCCC GACTCTGCCC TGCTTGTCAC GGCTTCTTAC GATACCAATG TGATTATGTG	660
GGACCCCTAC ACCGGCGAAA GGCTGAGGTC ACTCCACCAC ACCCAGGTG ACCCCGCCAT	720
GGATGACAGT GACGTCCACA TTAGCTCACT GAGATCTGTG TGCTTCTCTC CAGAAGGCTT	780
GTACCTTGCC ACGGTGGCAG ATGACAGACT CCTCAGGATC TGGGCCCTGG AACTGAAAAC	840
TCCCATTGCA TTTGCTCCTA TGACCAATGG GCTTGTCTGG CACATTTTTF CCACATGGTG	900
GATCATTTGC CACAGGGACA AGAGATGGCC ACGTCCAGTT CTGGACAGCT CCTAGGGTCC	960
TGTCCTCACT GAAGCACTTA TGCCGGAAAG CCCTTCGAAG TTTCCTAACA ACTTACCAAG	1020
TCCTAGCACT GCCAATCCCC AAGAAAATGA AAGAGTTCTT CACATACAGG ACTTTTAAAG	1080
CAACACCACA TCTTGTGCTT CTTTGTAGCA GGGTAAATCG TCCTGTCAAA GGGAGTTGCT	1140
GGAATAATGG GCCAAACATC TGGTCTTGCA TTGAAATAGC ATTTCTTTGG GATTGTGAAT	1200

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AGAATGTAGC AAAACCAGAT TCCAGTGTAC TAGTCATGGA TTTTTC

1246

## (2) INFORMATION FOR SEQ ID NO:23:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 422 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

ACCATGGTTC CAAGTCTCTT CCCCTGTGGT CAAGTTGCCC GAATGTTGGG CCCAAGTGCC	60
TTTTCTCTCT TGGGCTTCCC CTTCCTGACCT GCAGGACAGT TTTCCGGAGC CCATTTGGTA	120
TGAGGTATTA ATTAGCCTTA ACTAAATTAC ACGGGACTCA GAGGCCGTGC TCCTGACCGA	180
TCCAGACACT ATTTTTTTTT TTTTTTTTTT ACAATGGTGT GCATGTGCAG GAAATGACAA	240
ATTTGTATGT CAGATTATAC AAGGATGTAT TCTTAAACCG CATGACTATT CAGATGGCTA	300
CTGAGTTATC AGTGGCCATT TATTAGCATC ATATTATTTT GTATTTTCTC AACAGATGTT	360
AAGGTACAAC TGTGTTTTTC TCGATTATCT AAAAACCATA GTACTTAAAT TGAAAAAAA	420
AA	422

## (2) INFORMATION FOR SEQ ID NO:24:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2019 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GCCACGAGGC GGGGTCAGGG CGGAGGCTGA GGACCAAGTA GGCATGGCCG AGGGCGGGAC	60
CGGCCCCGAT GGACGGGCCG GCCCCGGACC CGCAGGTCCT AATCTGAAGG AGTGGCTGAG	120
GGAGCAGTTC TGTGACCATC CACTGGAGCA CTGTGACGAT ACAAGACTCC ATGATGCAGC	180
CTATGTAGGG GACCTCCAGA CCCTCAGGAA CCTACTGCAA GAGGAGAGCT ACCGGAGCCG	240
CATCAATGAG AAGTCTGTCT GGTGCTGCGG CTGGCTTCCC TGCACACCAC TGAGGATCGC	300
AGCCACTGCA GGCATGGGA ACTGTGTGGA CTTCCTCATA CGCAAAGGGG CCGAGGTGGA	360
CCTGGTGGAT GTCAAGGGGC AGACTGCCCT GTATGTGGCT GTAGTGAACG GGCACCTGGA	420
GAGCACTGAG ATCCTTTTGG AAGCTGGTGC TGATCCCAAC GGCAGCCGOC ACCACCGCAG	480
CACTCCTGTG TACCATGCCT YTCGTGTGGG TAGGGACGAC ATCCTGAAGG CTCTTATCAG	540
GTATGGGGCA GATGTTGATG TCAACCATCA TCTGAATTCT GACACCCGGC CCCCTTTTTC	600
ACGGCGGGCTA ACCTCCTTGG TGGTCTGTCC TCTATACATC AGTGCTGCCT ACCATAACCT	660
TCAGTGCTTC AGGCTGCTCT TGCAGGCTGG GGCAAATCCT GACTTCAATP GCAATGGCCC	720
TGTCAACACC CAGGAGTTCT ACAGGGGATC CCCTGGGTGT GTCATGGATG CTGTCTTGCG	780
CCATGGCTGT GAAGCAGCCT TCGTGAGTCT GTTGGTAGAG TTTGGAGCCA ACCTGAACCT	840
GGTGAAGTGG GAATCCCTGG GCCCAGAGGC AAGAGGCAGA AGAAAGATGG ATCCTGAGGC	900
CTTGCAGGTC TTTAAAGAGG CCAGAAGTAT TCCCAGGACC TTGCTGAGTT TGTGCCGGGT	960
GGCTGTGAGA AGAGCTCTTG GCAAATACCG ACTGCATCTG GTTCCCTCGC TGCCGCTGCC	1020
AGACCCCATTA AAGAAGTTTT TGCTTTATGA GTAGCATTCAT CATGCAGTGC TGAATGCAAT	1080
GTGGAAGCCG ATCACCTGCA GTGAAACTG ACACAGACTC TGGCATCCTG GGAACCATGG	1140
CCTGTGCTGC CAGCTTGATC CTTGGCTGTC AGTGAAGAAA AAACGGCTGT GTTCTCTTGG	1200
ACTGTGATTC TATCTCAGGT GCTTGGGCCA TCGAACGCTC CTTGAGTCAT TGTCAACTGA	1260

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GAGGCACATA CAAACTTAAT TTTGTTCCCTC TTCAGTCTCT CTGTTTGGG TTTCTCCTGG	1320
CAATGTGTGC AGCATGGGCT GAGCCTGGTG ATTGCCCTAG TGGGGAAGGC TTTTCTCTCC	1380
AGCCTATGCA TCTATTTATG TTCTTACTTT GCAATTTATT GTTCTTTTAA GGCTTGATAT	1440
CAAAACAGAA AGAGGTTTGT TAAGAAAAGA TATAGGGAGA AAGGAATTC GGTTCCTGTC	1500
ACTTGCTAGC CTGCTTTCCT TGCTTGGGTT TGTCTGTCTA TGCTGCCTGG TGCACATCCC	1560
TTCTCTTTGC TGCCACTGTT CTATTTTGGG AGTTGTCTTC CGTCTAAGAT GGCTTCTGGG	1620
GTTCTATCTT ATTGCACAGA GGTCCCAGAA CAGTGTTCAT AGGGCACCAT CTGCTCTGCC	1680
AAGGGTTTTT TCATGTCTTA CCTGCGGAT CTCACACAG TGGTTACCTT TAGGAGACCC	1740
ACCTGGAAC AACCATTAAG TGACTGCCCA CATTCAGATC AGGCACCATC TTAATAGTAC	1800
TCACTGCCAG TCCTCACAAG AGAAGATGAC ACGGGTGCTC TCTTCAGACA CTCCCATACA	1860
GGAAGTTGGA AAATGTCTTG GTCACCTGGG TTGTCCCAG GGTACAACTT CTGGGTGTTT	1920
CACTAARACC AGRATATCCT AGTTTTTTGG GTTGACTGTT CCTCCCCAC TTTCTTGAA	1980
NCCCAATGCC CNTTTGKTN GGTGCTTCC CTAAAKTT	2019

## (2) INFORMATION FOR SEQ ID NO:25:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 350 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Ala	Arg	Gly	Gly	Val	Arg	Ala	Glu	Ala	Glu	Asp	Gln	Val	Gly	Met	Ala
1				5						10				15	

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Glu Gly Gly Thr Gly Pro Asp Gly Arg Ala Gly Pro Gly Pro Ala Gly  
 20 25 30

Pro Asn Leu Lys Glu Trp Leu Arg Glu Gln Phe Cys Asp His Pro Leu  
 35 40 45

Glu His Cys Asp Asp Thr Arg Leu His Asp Ala Ala Tyr Val Gly Asp  
 50 55 60

Leu Gln Thr Leu Arg Asn Leu Leu Gln Glu Glu Ser Tyr Arg Ser Arg  
 65 70 75 80

Ile Asn Glu Lys Ser Val Trp Cys Cys Gly Trp Leu Pro Cys Thr Pro  
 85 90 95

Leu Arg Ile Ala Ala Thr Ala Gly His Gly Asn Cys Val Asp Phe Leu  
 100 105 110

Ile Arg Lys Gly Ala Glu Val Asp Leu Val Asp Val Lys Gly Gln Thr  
 115 120 125

Ala Leu Tyr Val Ala Val Val Asn Gly His Leu Glu Ser Thr Glu Ile  
 130 135 140

Leu Leu Glu Ala Gly Ala Asp Pro Asn Gly Ser Arg His His Arg Ser  
 145 150 155 160

Thr Pro Val Tyr His Ala Xaa Arg Val Gly Arg Asp Asp Ile Leu Lys  
 165 170 175

Ala Leu Ile Arg Tyr Gly Ala Asp Val Asp Val Asn His His Leu Asn  
 180 185 190

Ser Asp Thr Arg Pro Pro Phe Ser Arg Arg Leu Thr Ser Leu Val Val  
 195 200 205

Cys Pro Leu Tyr Ile Ser Ala Ala Tyr His Asn Leu Gln Cys Phe Arg  
 210 215 220

Leu Leu Leu Gln Ala Gly Ala Asn Pro Asp Phe Asn Cys Asn Gly Pro  
 225 230 235 240

Val Asn Thr Gln Glu Phe Tyr Arg Gly Ser Pro Gly Cys Val Met Asp  
 245 250 255

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Ala Val Leu Arg His Gly Cys Glu Ala Ala Phe Val Ser Leu Leu Val	
260	265 270
Glu Phe Gly Ala Asn Leu Asn Leu Val Lys Trp Glu Ser Leu Gly Pro	
275	280 285
Glu Ala Arg Gly Arg Arg Lys Met Asp Pro Glu Ala Leu Gln Val Phe	
290	295 300
Lys Glu Ala Arg Ser Ile Pro Arg Thr Leu Leu Ser Leu Cys Arg Val	
305	310 315 320
Ala Val Arg Arg Ala Leu Gly Lys Tyr Arg Leu His Leu Val Pro Ser	
325	330 335
Leu Pro Leu Pro Asp Pro Ile Lys Lys Phe Leu Leu Tyr Glu	
340	345 350

## (2) INFORMATION FOR SEQ ID NO:26:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 419 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GCATCCATGG CGGAGGGCGG CAGCACGACG GGCGGGCAGG GCCGGGCTCC GCAGGTCGTA	60
ATCTGAAGGA GTGGCTGAGG GAGCAATTTT GTGATCATCC GCTGGAGCAC TGTGAGGACA	120
CGAGGCTCCA TGATGCAGCT TACGTCGGGG ACCTCCAGAC CCTCAGGAGC CTATTGCAAG	180
AGGAGAGCTA CCGAGCCCGC ATCAACGAGA AGTCTGTCTG GTGCTGTGGC TGGCTCCCCT	240
GCACACCGTT GCGAATCGCG GCACTGCAG GCCATGGGAG CTGTGTGGAC TTCCTCATCC	300
GGAAGGGGGC CGAGGTGGAT CTGGTGGACG TAAAGGACA GACGGCCCTG TATGTGGCTG	360

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TGGTGAACGG GCACCTAGAG AGTACCCAGA TCCTTCTCGA AGCTGGCGCG GACCCCAAC 419

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 595 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

GAGCAAGAAG AAAACTGGAC CCTGAGGCCT TGCAAGTCTT TAAAGAGGCC AGAAGTGTTC	60
CCAGAACCTT GCTGTGTCTG TGCCGTGTGG CTGTGAGAAG AGCTCTTGCC AAAACCGGCT	120
TCATCTGATT CCTTCGCTGC CTCTGCCAGA CCCATAAAG AAGTTTCTAC TCCATGAGTA	180
GACTCCAAGT GCTGCGGTTG ATTCCAGTGA GGGAGAAAGT GATCTGCAGG GAGGTGGACA	240
CCGAGCCCTG AGTGCTGTGC TGCTGCTGGT CTCTGATGG CTGTGCTGC AGAAGATGTC	300
CTCGTAGACT GTCATTGCTC CTCAGGTGCC TGGCCCGCTG AACAGTCCTT GGGTCATTGT	360
CAGCTGAGAG GCTTATACTA AAGTTATTAT TSTTTTCCC AAGTTCTCTG TTCTGGATTT	420
TCAGTTGCAT ATTAATGTAA CGGGCCATGG GGTATGTACA TGTAGGGGCT GAGGTTGGAG	480
GCCTACTAAT TTCTGTAGG GAAGACTCCC AGCACTTCTG GAACTGTGCT TCTCTTTATT	540
TTTCTACTTC TCAATTTGAT GGTTCGATTA AAGCCTTCTA GTATCTCAAT GAAAA	595

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 896 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 4..396

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

CTG ATG TCC GCA ATT CTG AAG CTT GGA CAC CAC TGC TGG CTG CCT GTG	48
Met Ser Ala Ile Leu Lys Val Gly His His Cys Trp Leu Pro Val	
1 5 10 15	
ACA TCC GCT GTC AAT CCC CAA AGG ATG CTG AGG CCA CCA CCA ACC GCT	96
Thr Ser Ala Val Asn Pro Gln Arg Met Leu Arg Pro Pro Pro Thr Ala	
20 25 30	
GTT TTC AAC TGT GCC GCT TGC TGC TGT CTG TGG GGG CAG ATG CTG ATG	144
Val Phe Asn Cys Ala Ala Cys Cys Cys Leu Trp Gly Gln Met Leu Met	
35 40 45	
AAT ACA TAC CGT GTA GTT CAG CTT CCT GAG GAG GCC AAG GGC TTG GTG	192
Asn Thr Tyr Arg Val Val Gln Leu Pro Glu Glu Ala Lys Gly Leu Val	
50 55 60	
CCA CCA GAG ATT CTA CAG AAG TAC CAT GGA TTC TAC TCT TCC CTC TTT	240
Pro Pro Glu Ile Leu Gln Lys Tyr His Gly Phe Tyr Ser Ser Leu Phe	
65 70 75	
GCC TTG GTG AGG CAG CCC AGG TCG CTG CAG CAT CTC TGC CGT TGT GCG	288
Ala Leu Val Arg Gln Pro Arg Ser Leu Gln His Leu Cys Arg Cys Ala	
80 85 90 95	
CTC CGC AGT CAC CTG GAG GGC TGT CTG CCC CAT GCA CTA CCG CGC CTT	336
Leu Arg Ser His Leu Glu Gly Cys Leu Pro His Ala Leu Pro Arg Leu	
100 105 110	
CCC CTG CCA CCG CGC ATG CTC CGC TTT CTG CAG CTG GAC TTT GAG GAT	384
Pro Leu Pro Pro Arg Met Leu Arg Phe Leu Gln Leu Asp Phe Glu Asp	
115 120 125	
CTG CTC TAC TAGGCTTGCT GCCCTGTGAA CAAAGCAGAC CCCACCCCCA	433
Leu Leu Tyr	
130	

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CCCCAAGGGC ATCTCTCAGC AATGAATGAT GCAAGGCGGT CTGTCTTCAA GTCAGGAGTG      493
GACGCCCTGA TCCACACTTG AGAGAAGAGG CCAGATCAGC ACCYGGCTGG TAGTGATNGC      553
AGAGGGCACC TGTGCAGATC TGTGTGCGCA CTGGAAATCT CTAGGCTGAA GGCYAGAGCA      613
AATGCTGCAR GTGTTAGTCC TTGGGANGAG AGACAGANGG TGAGAAAGCA AGACAGAGGT      673
GAGAGTGCAC ATGTCAAGTG GTAGATTGCC TTAAGAGAAA GCTAAAAAAA GAAAAAGATT      733
CGGGCGAACT TCTTTAGGGG TAATGCTGCA GCGTGTTAAA CTGACTGACC AGCGTCCATA      793
TCTTTGGACC CTTCCCGGGT GAAAAAGCCC CTTCATCCTC CAGCGCTCCC CAAGGGTGCT      853
TAGCAATACC GGGTGCTTTT CTGCCGCAAA GTGAGTTACC AAA                        896

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## (2) INFORMATION FOR SEQ ID NO:29:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

```

Met Ser Ala Ile Leu Lys Val Gly His His Cys Trp Leu Pro Val Thr
  1              5              10              15
Ser Ala Val Asn Pro Gln Arg Met Leu Arg Pro Pro Pro Thr Ala Val
          20              25              30
Phe Asn Cys Ala Ala Cys Cys Cys Leu Trp Gly Gln Met Leu Met Asn
          35              40              45
Thr Tyr Arg Val Val Gln Leu Pro Glu Glu Ala Lys Gly Leu Val Pro
          50              55              60
Pro Glu Ile Leu Gln Lys Tyr His Gly Phe Tyr Ser Ser Leu Phe Ala
          65              70              75              80
Leu Val Arg Gln Pro Arg Ser Leu Gln His Leu Cys Arg Cys Ala Leu
          85              90              95

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Arg Ser His Leu Glu Gly Cys Leu Pro His Ala Leu Pro Arg Leu Pro  
                   100                  105                  110

Leu Pro Pro Arg Met Leu Arg Phe Leu Gln Leu Asp Phe Glu Asp Leu  
                   115                  120                  125

Leu Tyr  
           130

## (2) INFORMATION FOR SEQ ID NO:30:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 436 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

GTGGGGGGCGT CATCATGACC TCCTCTAGGG CTCTGCAACA TGACTCCTGT GGTGCAAATC 60

AACAAATTGT TCACTGATGA ATCCACAAGG ATCTCTGGGC CTACAACCAG GTCCTGGTCC 120

ACATGACTGT CGTCTTCGGA GAAGGCACCA CTCGCCCCCG GCAGGTACGG CTGACACCTC 180

CATGGGAGAA GACGTATCCA GGCAGCAGCT GCGCGGCCCT TCAAGAGGGC ACATCCCGTC 240

ATCTAAAGGC ACGGTGTACT GAAGGTAGTC CTGAGACATG AGTCCGATTA CTACAGGCAC 300

GTGTTCTTCC AGGTGGAGGC TCAGGTCCCC GGGTGAGCTG GGGCTGCAGC GGGACTCAGG 360

GCGCGGCTCT GGCTGCAGGT CTGCGAGCTC CCTGGGCTGT AGCTCCCGCA GATCCTTGCG 420

CACACCGTTG ACTGGT 436

## (2) INFORMATION FOR SEQ ID NO:31:

## (i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 2180 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

TTAATAGTAC CTACATAGTA GAAAATTATA ACTCCACTTT AAAACAATGT TTTCTTTCTA	60
TTCAAATCAA TTTAAACTT TTTATAACA TTAATGTTGC AAGAGAATCC AGTCCATTTA	120
TGAAAATTAG TTGACATCA AGTTCACCCA AGAAAATGTT GACTAAGCTA AAGAAATCAC	180
AGATAAACA TTTTACCAA AGGATAGGTA ACACACAAA AAATGCTATC ACAGGAAGCT	240
ATGATCACTT AATATTCTT TAATAATAAT TCTAGTTCCA TAGGTTTTCA TGTATGCCA	300
ATTTGTACCC GAGTTTAATT ACAGAAAAGG CAACAATTTT TAAATTGGTG GTATACATTT	360
CTTTACAATT TTTTAATGTA AGGCCATTTA TTAAATAGA CAAACTAGAA GATGAAAACG	420
AAGGCAACAG AAAAATTCAA CTTTTCACAA CCAAAGAAT TAGCACAACC TTAGAAATAA	480
TTTAGAAAAA AGTGTGTTA AAAGATATGT TGCAGATCTC CGTTCCATTA CCCAAGATTA	540
TGTCAATTCA CGATTCTAAA TAAATCTTTT TAAAGTAAGA GATTAAAAAC TCATCTTCAG	600
TGTATATGTA AATTCCGTGG TTTTATCACA CAGGTATGTT TATTCAACAC TGCTTTGGAA	660
ATGGACCATT TAAAAGGACA TGGCAATTTT CATTCTGTTA AGTTTCATTC AACCTTTACT	720
TAGGGGTGTA TTACCACATG AAATGTGCTT TTAATGCATA AAAATCACAG TGGATTAGCC	780
AGCAAAAGGG ACTGGGCGGG GGGGGCATTC AGGAGAATTT GATAATTCAC ATTGTGATTA	840
TTCTGCACAT TGATGAAACA TAATTCACAC CTCTAAACC TCAAGACTTC CCTTTTTTAA	900
AGAACCAAAA TAAACCAAG ACACCTTGCT GACACTTCCC CACCCCTAAA CAACTGATG	960
ACTCTTTTAC ACATAAACT GAAATAGTTA TGGCAGCAAA AGATTTTGAT GCGAATGAAA	1020

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GTTTGTAAC TGTATTTCAA TCTCTGTTC TTATCCCAA AGTGCAAGAT GCAGGTTCT	1080
CAATCTTTCA GTAGTGCTTC TCCTGTAAAT AATCCTTCAT TTTGTTTGGC AAAGGCAGTT	1140
TCTGAATTAA GTCTATTCTG GTATACTGAC GTATAACAAA ACGACACAGG TACTGCAACG	1200
AGCCACCTA TGAACCCCGG AACACTGGTT GGCAAGTTCT GACGGAAGTG CAGATTCCAG	1260
GCAGCGAGAC CTTGAATAAC AAAAAGCTCC CATTTTCAGA GTCCCTGATT GAATGCTCCA	1320
ATTAGATCAA CTATGGACGT ATGTCCTTCC ACATCGGCTG TTCATAAAAG CTAAACCTAC	1380
CATTTGAGTG CTCAATTCTA GTGTGAAGTG TTTTACCATG GGAGCGAAAG TCACAGCTTA	1440
AAAGGTAAAG GTCGTCAGAA CTGTCCCGAA CAAGAAAAGA ACCATCTGGC ACGTTTGCTA	1500
GCTTCCCTTC TGCTCCCAA CGGTGATTG GTCCCCAGTA CCATCCTTGC TTTGCAAGTT	1560
TTTTGAGCTC CTCTGTAAAG CTGTACAA CCATGGGACC ACTACTTTC ACTGAGTCAT	1620
AAACTCTTGC AAGCCAGGA GCAGAGTTG GATCAAAATT CAAATGACAG CGCATAACTT	1680
TCAGCCACGT GGGGCTTCT GTCCAGTGAG TCCACTGAAA GTTCCCTTTT GGGATTGGA	1740
TTATTCCTGC ATTGGAGTAA CCAATGGTGA AGATTGGAGG GACATCCATC GTGAACCCGC	1800
TCTCCGGGT TCTGCAACAT GACTCCCGTG GTGCCAATCA ACAAGCCATT CACCGGACTG	1860
ATCCACGAAG ATCTCTGGG GACAACTAG GTCTGGTCT ACCTGACTCT CATCTCGGG	1920
GAAAGCGGC CCTCCACTT GAGGAGGAAC CGCAGAGACT TCCATGGGAG AAGAGCTGTC	1980
CAGACAATAG CTCCGTGATC CTTCAAAGG ATACATCCCC TCATCTAAAG GCACAGTATA	2040
CTGAATGTAG TCCTGAGGCA TAAGTCCAT AACGACAGGC ACATGTTTAT CCAGGTGAAG	2100
ATGCAGGTCT CCATTATGAG AAGCCGAGCT CTTGAGTGA TTGGCTTGCT CCTGGCACGT	2160
GCTCTCAGAC TGGAGGTCT	2180

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 2649 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

GGCAGGAGGC TGTGTCCAGC ACACAGAGAG GGCCCGGCCA TCTGCTTTGG TTCAGAGCCC	60
TGTGTCTGTC TGTCACTTAG ACTCTTCCTC CCGGCTCGCA GCTCACCCCTC CATCCTCCTT	120
ACTGGCTCCA GCATGACTCG CTCTCTTAT GCAGAGTACT TTGCTCTGTT TCACTCTGGC	180
TCTGCACCTT CCAGGTCCCC TTCGTCTCCC GAGAAGCCAC CGGCCCCGCG ACCCCTGGGT	240
CTGTTCCAAG GGGTCATGCA GAAGTATAGC AGCAACCTGT TCAAGACCTC CCAGATGGCG	300
GCTATGGACC CCGTCTGAA GGCCATCAAG GAAGGGGATG AAGAGGCCTT GAAGATCATG	360
ATCCAGGATG GGAAGAATCT TGCAGAGCCC AACAAGGAGG GCTGGCTGCC GCTCCACGAG	420
GCTGCCTACT ATGGCCAGCT GGGCTGCCTG AAAGTCTTGC AGCAAGCCTA CCCAGGGACC	480
ATTGACCAAC GCACACTGCA GGAAGAGACA GCATTATACC TGGCCACATG CAGAGAACAC	540
CTGGATTGCC TCCTGTCCCT GCTCCAGGCG GGGCCAGAGC CTGACATCTC TAACAAATCC	600
AGGGAGACTC CACTTTACAA AOCCTGTGAG CGCAAGAACG CGGAGGCGGT GAGGATATTG	660
GTGCCATACA ACCCAGACGC CAACCACGCG TGTAACAGGG GCTGGACCGC ACTGCACGAG	720
TCTGTCTCCC GCAATGACCT GGAAGTCATG GAGATCCTAG TGACTGGCGG GGCCAAGGTG	780
GAGGCCAAGA ATGTCTACAG CATCACCCCT TTGTTTGTGG CTGCCCAGAG TGGGCAGCTG	840
GAGGCCCTGA GGTTCCTGGC CAAGCATGGT GCAGACATCA ACACGCAGGC CAGTGACAGT	900
GCATCAGCCC TCTACGAGGC CAGCAAGAAT GAGCATGAAG ACGTGGTAGA GTTCTCTCTC	960
TCTCAGGGCG CCGATGCTAA CAAAGCCAAC AAGGACGGCC TGCTCCCCCT GCATGTTGCC	1020

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TCCAAGAAGG GCAACTATAG AATAGTGCAG ATGCTGCTGC CTGTGACCAG CCGCACGCCG	1080
GTGCGCCGTA GCGGCATCAG CCGCTGCAC CTAGCGGCCG AGCGCAACCA CGACCGGGTG	1140
CTGGAGGCCG TGCTGGCCGC GCGCTTCGAC GTGAACGCAC CTCTGGCTCC CGAGCGCGCC	1200
CGCCTCTAAG AGGACCGCCG CAGTTCTGCG CTCTACTTCG CTGTGGTCAA CAACAATGTG	1260
TACGCCACCG AGCTGTTGCT GCTGGCGGGC GCGGACCCCA ACCGCGATGT CATCAGCCCT	1320
CTGCTCGTGG CCATCCGCCA CGGCTGCCTG CGCAACATGC AGCTGCTGTT GGACCATGGC	1380
GCCAACATCG ACGCCTACAT CGCCACTCAC CCCACCGCCT TTCCAGCCAC CATCATGTTT	1440
GCCATGAAGT GCCTGTCGTT ACTCAAGTTC CTATGAGACC TCGGCTGCGA TGGCGAGCCC	1500
TGCTTCTCCT GCCTGTACGG CAACGGGCCG CACCACCCGC CCCCGACCT GSCCGCTTCC	1560
ACGACGCACC CGTGGACGAC AAGGCACCTA GCGTGGTGCA GTTCTGTGAG TTCCTGTGG	1620
CCCCGGAAGT GAGCCGCTGG GCGGGACCCA TCATCGATGT CCTCTGGAC TATGTGGGCA	1680
ACGTCCAGCT GTGCTCCCGG CTGAAGGAGC ACATCGACAG CTTTGAGGAC TGGGCTGTCA	1740
TCAAGGAGAA GGCAGAACCT CCGAGACCTC TGGCTCACCT CTGCCGGCTG CGGCTTCGGA	1800
AGGCCATAGG AAAATACCGG ATAAACTCC TGGACACACT GCCGCTTCCC GGCAGGCTAA	1860
TCAGATACTT GAAATATGAG AATACACAGT AACCAGCCTG GAGAGGAGAT GTGCCCTTCA	1920
GACTGTTTCC GGGACGCCCC AGGTGGCCTG CATCCAGGAC CCCCTGGGGT CAGAACAGGT	1980
GTGACCTTGC TGCTTCTTTG CTGGAGCTTC ACCCAAAGTG AGAACCTGAT GTGGGGAGTG	2040
GACGTGGAAC CTCTGCTTTC ACACTGTCAG CGGATCGCAG ACCCGCTCTG CTTCTGGCCA	2100
TAGCCAGAGA CCTTCAACCT GGGGCCAGGG GAGAGCTGGT CTGGGCAAGG TGGCCCAGGC	2160
AGGAATCCTG GCCTTAAGCT GGAGAACTTG TAGGAATCCC TCACTGGACC CTCAGCTTTC	2220
AGGCTGCGAG GGAGACGCCC AGCCCAAGTA TTTTATTTCC GTGACACAAT AACGTTGTAT	2280
CAGAAAAAAA AAAAACATG GCGCAGCTT ATTCCTTAGT AGGGTATTTA CTTGCATGCG	2340
CGCTTAAAGC TACTGGAAAC ATGCGTTCCA CTATGCTTGA GAATCCGCTT GCACTGGTAA	2400



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ACGAGAGCCG ACGTGCTTCA AGGTTGGATT TTTGGTTGCC CCTTTGGCGT TCCGCGGCTT	2460
TGTCCGACGT AATTGACCCC GTGTTTGTGTC ACTTTCGAGT GTTCCGACTA TTGGGGGGCT	2520
TTTGGTTGTC CCAAAAATTG TGGGTGGTGT GCGGACGCCA CGAGAAGTGG TTCATGGGCG	2580
ATAATCATTA CTGGAGAATG TAGAGCGGCG GTTTTACGAA TAAATATTTT TTAAGCCGCC	2640
TTCCCAAAA	2649

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 495 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

CCTCCTGAGA GTTCGCCGGC CCGGGCCCAA TGGGTTGTTT CAAGGGGTCA TGCAGAAATA	60
CAGCAGCAGC TTGTTCAAGA CCTCCCAGCT GCGGCCTGCG GACCCCTGA TAAAGGCCAT	120
CAAGGATGCG ATGAAGAGGC CTTGAAGACC ATGATCAAGG AAGGAAGAA TCTCGCAGAG	180
CCCAACAAGG AGGGCTGGCT GCGCTGCAC GAGGCCGAT ACTATGGCCA GGTGGGCTGC	240
CTGAAAGTCC TGCAGCGAGC GTACCCAGGG ACCATCGACC AGCGCACCT GCAGGAGGAA	300
ACAGCCGTTT ACTTGGCAAC GTGCAGGGGC CACCTGGACT GTCTCCTGTC ACTGCTCCAA	360
GCAGGGGCAG AGCGGGACAT CTCCAACAAA TCCCGAGAGA ACCGCTCTAC AAAGCCTGTG	420
AGCGCAAGAA CCGGAAGCC GTGAAGATTC TTGGTGCAGC ACAACGCAGA CACCAACAAC	480
GCTGCAACCG GGCTG	495

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 709 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

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GTGCAGCTCT GCTCGGGCT GAAGGAACAC ATCGACAGCT TTGAGGACTG GGCCGTCATC      60
AAGGAGAAGG CAGAACCTCC AAGACCTCTG GCTCACCTTT GCCGACTGCG GGTTCGAAAG      120
GCCATTGGGA AATACCGTAT AAAACTCCTA GACACCTTGC CGCTCCCAGG CAGGCTGATT      180
AGATACCTGA AATACGAGAA CACCCAGTAA CTGGGGCCAC GGGGAGAGAG GAGTAGCCCC      240
TCAGACTCTT CTACTAAGT CTCAGGACGT CGGTGTTCCTT AACTCCAAGG GGACCTGCTG      300
ACAGACGAGG CTGCAGGCTG CCTCCCTCTC AGCCTGGACA GCTACCAGGA TCTCACTGGG      360
TCTCAGGGCC CAGAGCTTTG GCCAGAGCAG AGAACAGAAT GTGTCAAGGA GAAGAATCAT      420
TTGTTTACAA ACTGATGAGC AGATCCCAGA CCTTCTCTAC CTCAGGAAT GGCAGAAACC      480
TCTATTCTTG GGGCCAGGGC AGAGCTTGAG GTGTCTGGG GAAGGTGGTG CTCAGAGCCT      540
TCCCTGTGCC CTTCACCTTG TTCTGCAAAA CTCACCACTT GACTTCAGAG CTTTCTCTCC      600
AAAGACTAAG ATGAACACGT GGGCCAAGGT AGGGGGTAGG GGGAGCCTGG GTCTTGAGAG      660
GCTTTGTTAA GTATTAAATAT AATAAATGTT ACACATGTGA AAAAAAAAAA      709

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(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 848 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..624

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

TTG GAG AAG TGT GGT TGG TAT TGG GGG CCA ATG AAT TGG GAA GAT GCA	48
Leu Gln Lys Cys Gly Trp Tyr Trp Gly Pro Met Asn Trp Glu Asp Ala	
1 5 10 15	
GAG ATG AAG CTG AAA GGG AAA CCA GAT GGT TCT TTC CTG GTA CGA GAC	96
Gln Met Lys Leu Lys Gly Lys Pro Asp Gly Ser Phe Leu Val Arg Asp	
20 25 30	
AGT TCT GAT CCT CGT TAC ATC CTG AGC CTC AGT TTC CGA TCA CAG GGT	144
Ser Ser Asp Pro Arg Tyr Ile Leu Ser Leu Ser Phe Arg Ser Gln Gly	
35 40 45	
ATC ACC CAC CAC ACT AGA ATG GAG CAC TAC AGA GGA ACC TTC AGC CTG	192
Ile Thr His His Thr Arg Met Glu His Tyr Arg Gly Thr Phe Ser Leu	
50 55 60	
TGG TGT CAT CCC AAG TTT GAG GAC CGC TGT CAA TCT GTT GTA GAG TTT	240
Trp Cys His Pro Lys Phe Glu Asp Arg Cys Gln Ser Val Val Glu Phe	
65 70 75 80	
ATT AAG AGA GCC ATT ATG CAC TCC AAG AAT GGA AAG TTT CTC TAT TTC	288
Ile Lys Arg Ala Ile Met His Ser Lys Asn Gly Lys Phe Leu Tyr Phe	
85 90 95	
TTA AGA TCC AGG GTT CCA GGA CTG CCA CCA ACT CCT GTC CAG CTG CTC	336
Leu Arg Ser Arg Val Pro Gly Leu Pro Pro Thr Pro Val Gln Leu Leu	
100 105 110	
TAT CCA GTG TCC CGA TTC AGC AAT GTC AAA TCC CTC CAG CAC CTT TGC	384
Tyr Pro Val Ser Arg Phe Ser Asn Val Lys Ser Leu Gln His Leu Cys	
115 120 125	
AGA TTC CGG ATA CGA CAG CTC GTC AGG ATA GAT CAC ATC CCA GAT CTC	432
Arg Phe Arg Ile Arg Gln Leu Val Arg Ile Asp His Ile Pro Asp Leu	
130 135 140	

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CCA CTG CCT AAA CCT CTG ATC TCT TAT ATC CGA AAG TTC TAC TAC TAT 480  
 Pro Leu Pro Lys Pro Leu Ile Ser Tyr Ile Arg Lys Phe Tyr Tyr Tyr  
 145 150 155 160

GAT CCT CAG GAA GAG GTA TAC CTG TCT CTA AAG GAA GCG CAG CGT CAG 528  
 Asp Pro Gln Glu Glu Val Tyr Leu Ser Leu Lys Glu Ala Gln Arg Gln  
 165 170 175

TTT CCA AAC AGA AGC AAG AGG TGG AAC CCT CCA CGT AGC GAG GGG CTC 576  
 Phe Pro Asn Arg Ser Lys Arg Trp Asn Pro Pro Arg Ser Glu Gly Leu  
 180 185 190

CCT GCT GGT CAC CAC CAA GGG CAT TTG GTT GCC AAG CTC CAG CTT TGAAGAACCA  
 631  
 Pro Ala Gly His His Gln Gly His Leu Val Ala Lys Leu Gln Leu  
 195 200 205

AATTAAAGCTA CCATGAAAAG AAGAGCAAAA GTGAGGGAAC AGGAAGGTTG GGATTCTCTG 691

TGCAGAGACT TTGGTTCCCC ACGCAAGCCC TGGGGCTTGG AAGAAGCACA TGACCGTACT 751

CTGCGTGGGG CTCCACCTCA CACCCACCCC TGGGCATCTT AGGACTGGAG GGGCTCCTTG 811

GAAAACTGGA AGAAGTCTCA ACACTGTTTC TTTTCA 848

## (2) INFORMATION FOR SEQ ID NO:36:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 207 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Leu Glu Lys Cys Gly Trp Tyr Trp Gly Pro Met Asn Trp Glu Asp Ala  
 1 5 10 15

Glu Met Lys Leu Lys Gly Lys Pro Asp Gly Ser Phe Leu Val Arg Asp  
 20 25 30

Ser Ser Asp Pro Arg Tyr Ile Leu Ser Leu Ser Phe Arg Ser Gln Gly  
 35 40 45

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Ile Thr His His Thr Arg Met Glu His Tyr Arg Gly Thr Phe Ser Leu
  50                      55                      60

Trp Cys His Pro Lys Phe Glu Asp Arg Cys Gln Ser Val Val Glu Phe
  65                      70                      75                      80

Ile Lys Arg Ala Ile Met His Ser Lys Asn Gly Lys Phe Leu Tyr Phe
                      85                      90                      95

Leu Arg Ser Arg Val Pro Gly Leu Pro Pro Thr Pro Val Gln Leu Leu
          100                      105                      110

Tyr Pro Val Ser Arg Phe Ser Asn Val Lys Ser Leu Gln His Leu Cys
          115                      120                      125

Arg Phe Arg Ile Arg Gln Leu Val Arg Ile Asp His Ile Pro Asp Leu
          130                      135                      140

Pro Leu Pro Lys Pro Leu Ile Ser Tyr Ile Arg Lys Phe Tyr Tyr Tyr
          145                      150                      155                      160

Asp Pro Gln Glu Glu Val Tyr Leu Ser Leu Lys Gln Ala Gln Arg Gln
          165                      170                      175

Phe Pro Asn Arg Ser Lys Arg Trp Asn Pro Pro Arg Ser Glu Gly Leu
          180                      185                      190

Pro Ala Gly His His Gln Gly His Leu Val Ala Lys Leu Gln Leu
          195                      200                      205

```

## (2) INFORMATION FOR SEQ ID NO:37:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 464 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

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GTTCCAAGCC TAACCCATCT TTGTCGTTTG GAAATTCGGG CCAGTCTAAA AGCAGAGCAC      60
CTTCACTCTG ACATTTTCAT CCATCAGTTG CCACTTCCCA GAAGTCTGCA GAACTATTTG     120
CTCTATGAAG AGGTTTTAAG AATGAATGAG ATTCTAGAAC CAGCAGCTAA TCAGGATGGA     180
GAAACCAGCA AGGCCACCTG ACACAGGTCC TTTAATTCCTG TTTAGTCACA AAAGACGGCT     240
TGTGTGACTG TTTGGATTTG GTGATCAAAT GTCCATGTTT ACAGTTGCTT TTCCAGTTT      300
GTGTCTTTCC CAATATTCTG AACCTTATCC ATCTTGCTT ACTCAGTTTT ATTTCTAGTG     360
CACTTTGTTG TGTATTATTT GTTTACCTGA CCATTTTCTA CTTTATTCTG CTAATAAACT     420
GTAATTTCTG AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAA                      464

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(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 747 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

```

GGGGATCGBA AGCGGGGGCT TCTGGGACGC AGCTCTGGAG ACGCGGCCTC GGACCAGCCA      60
TTTCGGTGTA GAAGTGGCAG CACGGCAGAC TGGTCAAACA AATGGATTTT ACAGAGGCTT     120
ACGCGGACAC GTGCTCTACA GTTGGACTTG CTGCCAGGGA AGGCAATGTT AAAGTCTTAA     180
GGAAACTGCT CAAAAGGGC CGAAGTGTG ATGTTGCTGA TAACAGGGGA TGGATGCCAA     240
TTCATGAAGC AGCTTATCAC AACTCTGTAG AATGTTTGCA AATGTTAATT AATGCAGATT     300
CATCTGAAAA CTACATTAAG ATGAAGACCT TTGAAGGTTT CTGTGCTTTG CATCTCGCTG     360
CAAGTCAAGG ACATTGGAAA ATCGTACAGA TTCTTTTAGA AGCTGGGGCA GATCCTAATG     420
CAACTACTTT AGAAGAAACG ACACCATTGT TTTTAGCTGT TGAAAATGGA CAGATAGATG     480

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TGTTAAGGCT GTTGCTTCAA CACGGAGCAA ATGTTAATGG ATCCCATTCCT ATGTGTGGAT	540
GGAACTCCTT GCACCAGGCT TCTTTTCAGG AAAATGCTGA GATCATAAAA TTGCTTCTTA	600
GAAAAGGAGC AAACAAGGAA TGCCAGGATG ACTTTGGAAT CACACCTTTA TTTGTGGCTG	660
CTCAGTATGG CCAAGCTAGA AAGCTTTGAA GCATACTTAT TTCATCCGGG TGCAAATGTC	720
AATTGTCAAG CCTGGACAA AGCTACC	747

(2) INFORMATION FOR SEQ ID NO:39:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1018 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

CACAAATGGG ACCATACAAA AATCTTGGAC TTGTTAATAA CCACTTACTA ACCGGGACCT	60
GTGACACTGG GCTAAACAAA GTAAGTCCCT GTTTACTCAG CAGTGTTTGG GGGACATGAA	120
GGATTGCCCTA GAAATATTAC TCCGGAATGG TCTACAGCCC AGACGCCCAG GCGTGCCCTTG	180
TTTTTGGAAT CAGTTCTCCT GTGTGCATGG CTTTCCAAAA GGAGGTGGAG CTGTAGTTCT	240
TTGGAATTGT GAACATTCTT TTGAAATATG GAGCCCAGAT AATGAACCTT CATTTGGCAT	300
ACTGCCTGAA GTACGAGAAG TTTTCGATAT TTCGCTACTT TTTGAGGAAA GGTTCCTCAT	360
TGGGACCATG GAACCATATA TATGAATTTG TAAATCATGC AATTAAAGCA CAAGCAAAAT	420
ATAAGGAGTG GTTCCACAT CTTCTGGTTG CTGGATTGGA CCCACTGATT CTACTGTGCA	480
ATTCTTGGAT TGACTCAGTC AGCATTGACA CCCTTATCTT CACTTTGGAG TTTACTAATT	540
GGAAGACACT TGCACCAGCT GTTGAAAGGA TGCTCTCTGC TCGTGCCTCA AACGCTTGA	600
TTCTACAGCA ACATATTGCC CACTGTTCCA TCCCTGACCC ATCTTTGTGG TTTGGAAATT	660

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CGGTCCAGTC TAAAATCAGA ACGTCTACGG TCTGACAGTT ATATTAGTCA GCTGCCACTT	720
CCCAGAAGCC TACATAATTA TTGCTCTAT GAAGACGTTT TGAGGATGTA TGAAGTTCCA	780
GAACTGGCAG CTATTCAAGA TGGATAAATC AGTGAAACTA CTTAACACAG CTAATTTTTT	840
TCTCTGAAAA ATCATCGAGA CAAAAGAGCC ACAGAGTACA AGTTTTTATG ATTTTATAGT	900
CAAAAGATCA TTATTGATTG TCAGATAGGT TAGGTTTTGG GGGGCCAGTA GTTCAGTGAG	960
AATGTTTATG TTTACAACTA GCCTTCCCAG TAAAAAATAA AAAAAAATAA AAAAAATAA	1018

## (2) INFORMATION FOR SEQ ID NO:40:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1897 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

CGGGGGGCTG GGACCTGGGG CGTAACCGTC TCTACCACGA CGGCAAGAAC CAGCCAAGTA	60
AABCATACCC AGCCTTTCTG GAGCCGGACG AGACATTCAT TGTCCCTGAC TCCTTTTTTCG	120
TGGCCCTGGA CATGRATGAT GGGACCTTAA GTTTCATCGT GCATGGACAG TACATGGCAG	180
TGGCTTTCCG GGGACTCAAG GGTAAAAGC TGTATCCTGT AGTGAGTGCC GTCTGGGGCC	240
ACTGTGAGAT CCGCATGCGC TACTTGAACG GACTTGATCC TGAGCCCCTG CCACTCATGG	300
ACCTGTGCGG GCGTTCGGTG CGCCTAGCGC TGGGAAAAGA GCGCCTGGGT GCCATCCCCG	360
CTCTGCCGCT ACCTGCCCTC CTCAAAGCCT ACCTCCTCTA CCAGTGATCC ACATCCCAGG	420
ACCGCCATAC GACAGCCATC TGGTGCCAAR TCACTGAGCC CGTTGGGGTC CGCCGACCCC	480
TGCGCCTGGG ATGGAAGCCC ACCTCAGCCA TGGGCAGACG TGCCCCCTCA TCCTACCGGC	540

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TGCTCTGCT GGGGGAACCT ATGCCAACGG ACTTCTCCCT TCCCAACACT GGCTGAAGCA	600
GCAGCACCCA GGGCCTTCCC TGAACCAGAT GCAGAGAATA AACTATGAAA ACCTCTCTCA	660
GGCGCCTTCT GCTCTCAGGT GGAGTGGGCT GCGCCCCACT CTCTGCAGAG AGAGGCTACA	720
CCCACCTGGG GGGTCCTGGG AGGTAAGACT AGTAGGAGGT GCCAGGGCTG ARTCCAAAAG	780
CAGGAATGGC CAGGAMCAGG CCATACAGAT GAAGCTCAGG ATGTCACATA CCATGGACAM	840
TGAGACAGAA CCCCAGTTG GAMPCCCTT GGGCCAACGA GTGCCAGCTT TAATGTCAGC	900
TGCMGGTGCT CTGTGGCCTG TATTTATCT TTAACAGTA GCAAAGGCCA TTTATTTATT	960
CCACTTAGAA AGGAAACCTT GGTGGGTGGY TTCCTCGAT GTGCTTTCCC CCACCTCCCT	1020
GGATGTGTG TGCCACACCT GTCCTGTTC CAGGCCAGGA CTGTGCCACA TGAGCTGGTG	1080
TGCACAGATA CACGTATGTC GTGTGCATG ACCCTGACT AGTTCCCTAG TAGCCCTCCA	1140
CCAAGCACCA GAGCAGACCC CAAGAGAGGC CCGTGCAAGT CCCCATGTCC CCAGGTCCCT	1200
GCTTCTGTTG CCTTGGGACT CATAACCCG CACACGTGTT TCAGCCTCTT GACTTCCATG	1260
AGCTTCGAAT TTGCCCCCG ATTCTTCTGA TATTTCCTAT TGGCATCCTC CAAAGCTCTG	1320
GGCCTGGAGG GCATTAGGAC ACATGGAATG AGTGGGGTCT CCAGCCCCCTG GGAAAGCCAC	1380
TGGCAAGGCA GGATTAGAAA GACCAAGAGC AGGGTGGGGC GCCATGAAGC CTGTATGCTT	1440
CTCAGGCTCA AGACCCCGCC ACACACCCAC TCAAGCCTCA GAAGTGGTGT GTAGGSCACC	1500
CCCAGGAGAG GAATGCCTGT CCTAGCAGCA CGTACATGGA GCACCCACAC TGTGCTCCAG	1560
CCCTCTGGCT GTTCTCTTG CTCTAGAAAC AACTCCCTAC ATTGGGAATG TAGCCATTTG	1620
GTAGAGGACT TGCTTAGCCT GCAGGAAGCT CACGTTCAT CCCCTGCACC AAGGAGAATC	1680
AAAGCTCAGG AGGCTGAGGC AGGAGGATTG CTGTCACTGG TGTACAGAGG TCATGGCCAT	1740
CCTGGGCTAT ATTAAACCTT GTCCTTTAAG AAAAAGAAAA GAAATCAACT TCCATTGAAT	1800
CTCAGTCTTG CTCATTTCTG CACAGGTACA ATAGATGACT TRATTTGTTG AAAAATGKTT	1860
AATATATTTA CMTATATATA TATTTGTAAG AAGCATT	1897

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## (2) INFORMATION FOR SEQ ID NO:41:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

Gly	Gly	Trp	Asp	Leu	Gly	Arg	Asn	Arg	Leu	Tyr	His	Asp	Gly	Lys	Asn
1				5					10					15	
Gln	Pro	Ser	Lys	Thr	Tyr	Pro	Ala	Phe	Leu	Glu	Pro	Asp	Glu	Thr	Phe
			20					25					30		
Ile	Val	Pro	Asp	Ser	Phe	Phe	Val	Ala	Leu	Asp	Met	Xaa	Asp	Gly	Thr
	35						40					45			
Leu	Ser	Phe	Ile	Val	Asp	Gly	Gln	Tyr	Met	Gly	Val	Ala	Phe	Arg	Gly
	50					55					60				
Leu	Lys	Gly	Lys	Lys	Leu	Tyr	Pro	Val	Val	Ser	Ala	Val	Trp	Gly	His
65					70					75				80	
Cys	Glu	Ile	Arg	Met	Arg	Tyr	Leu	Asn	Gly	Leu	Asp	Pro	Glu	Pro	Leu
			85					90						95	
Pro	Leu	Met	Asp	Leu	Cys	Arg	Arg	Ser	Val	Arg	Leu	Ala	Leu	Gly	Lys
		100						105					110		
Glu	Arg	Leu	Gly	Ala	Ile	Pro	Ala	Leu	Pro	Leu	Pro	Ala	Ser	Leu	Lys
		115					120					125			
Ala	Tyr	Leu	Leu	Tyr	Gln										
		130													

## (2) INFORMATION FOR SEQ ID NO:42:

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- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 265 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

AAGGGTAAAA AACTGTATCC TGTAGTGAGT GCCGTCTGGG GCCACTGTAG ATCCGAATGC	60
GCTACTTGAA CGGACTCGAT CCGGAGACTG CCGCTCATGG ATTTGTGCCG TCGCTCGGTC	120
CGCTGCCCC TGGGAGGGA GCGCCTGGG GAGAACCACA CCGCCGCTG CCGGCTTCCC	180
TCAAGGCCTA CTPCCTCTAC CAGTGACGTT CGCCATCATA CCGCCAGCCG GACAGCCACC	240
TGCTGCCAAC TCACTGAGCC GCCTG	265

(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2438 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

AAGTGGCGGC GTTCCCTGGA GAGCAGGCGG AGGCAGCGGC AAGTCTGACT CTGGGCTGAC	60
CGTGGAGCCG GGGCGGGGCG TGACAGCCAG GCCTCCGCCT GGCGGGAGCC GCACGAGGAG	120
CGCGAGTGGC CGGGCCTCTC TTCCGCGCTT GAGCGAGCGC CGGGTGATGG CGGTGGTGAT	180
GGCGGCAGGC GCTCGGACAG CTCCCTTGA GCTGAGCTCG GAGAGATCCG TCCAGAAAGT	240

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GCCCAGAAGA AACTTCCCTCT TAGAAAAGCT GAAAAACACA RTATTTATAA CACTGGAAAT	300
TGTAAAGAAT TTGTTTAAAA TGGCTGAAAA CAATAGTAAA AATGTAGATG TACGGCCTAA	360
AACAAGTCGG AGTCGAAGTG CTGACAGGAA GGATGGTTAT GTGTGGAGTG GAAAGAAGTT	420
GTCTTGGTCC AAAAAGAGTG AGAGTTGTTT TGAATCTGAA GCCATAGGTA CTGTTGAGAA	480
TGTTGAAATT CCTCTAAGAA GCCAAGAAAG GCAGCTTAGC TGTTCGTCCA TTGAGTTGGA	540
CTTAGATCAT TCCTGTGGGC ATAGATTTTT AGGCGGATCC CTTAAACAGA AACTGCAAGA	600
TGCGGTGGGG CAGTGTTTTC CAATAAGAA TTGTAGTGGC CGACACTCTC CAGGGCTTCC	660
ATCTAAAAGA AAGATTCATA TCAGTGAAGT CATGTTAGAT AAGTGCCTT TCCCACCTCG	720
CTCAGATTTA GCGTTAGGT GGCATTTTAT TAAACGACAC ACTGTTCTTA TGAGTCCCAA	780
CTCAGATGAA TGGGTGAGTG CAGACCTGTC TGAGAGGAAA CTGAGAGATG CTCAGCTGAA	840
ACGAAGAAAC ACAGAAGATG ACATACCCTG TTCTFCACAT ACCAATGGCC AGCCTTGTGT	900
CATAACTGCC AACAGTGCTT CGTGACAGG TGCFCACATA ACTGGTTCTA TGATGAACTT	960
GGTCACAAAC AACAGCATAG AAGACAGTGA CATGGATTCA GAGGATGAAA TTATAACGCT	1020
GTGCACAAGC TCCAGAAAAA GGAATAAGCC CAGGTGGGAA ATGGAAGAGG AGATCCTGCA	1080
GTGGAGGCA CCTCCTAAGT TCCACACCCA GATCGACTAC GTCCACTGCC TTGTTCCAGA	1140
CCTCCTTCAG ATCAGTAACA ATCCGTGCTA CTGGGGTGTC ATGGACAAAT ATGCAGCCGA	1200
AGCTCTGCTG GAAGGAAAGC CAGAGGGCAC CTTTCTACTT CGAGATTCAG CGCAGGAAGA	1260
TTATTTATTC TCTGTTAGTT TTAGACGCTA CAGTCGTTCT CTTCATGCTA GAATTGAGCA	1320
GTGGAATCAT AACTTTAGCT TTGATGCCCA TGATCCTTGT GTCTTCATT CTUCTGATAT	1380
TACTGGGCTC CTGGAACACT ATAAGGACCC CAGTGCCTGT ATGTTCTTTG AGCCGCTCTT	1440
GTCCACTCCC TTAATCCGGA CGTTCCCTT TTCCTTGCAG CATATTTGCA GAACGGTTAT	1500
TTGTAATTGT ACGACTTACG ATGGCATCGA TGCCCTTCCC ATTCTTCCG CTATGAAATT	1560
GTATCTGAAG GAATACCAAT ATAAATCAAA AGTTAGGTTA CTCAGGATTG ATGTGCCAGA	1620

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GCAGCAGTGA TCGCGAGAGG TTAGAATGTC GACCTGCATA CATATTTTCA TTTAATATTT	1680
TATTTTCTTT ATGCCTCTTT GAATTTTGT ACAAAGSCAG TTGAATCAAA TAAAACTGTG	1740
CCCTAAGTTT TAATTCCAGA TCAATTTATT TTTTTATGA TACACTTGT ATATATTTT	1800
AAGCAGGTGT TTGGTTTGT TTTTACCATA TAAATTTACA TATGGGCCAG GCATATTTAC	1860
AATTTCAAGG CATTGCATAT ACATTTGAAT ATTCTGTATT TTTTAAATAA TCTTTTGTTC	1920
TTTCCTATGT GTGAAATATT TTGCTAATCT ATGCTATCAG TATTCTTGTG TGACCGAATA	1980
GTTACCTATT CTCTTTTCAT CTTGAAGATT TTCAGTAAAG AGTGTGTAA TCAATCCATT	2040
ATAATCTAAT TGACTTTTGT AATTTGCCAA TAGGAGTGT AAACAACAAA ATGATTTAAA	2100
ATGAAACTTA ATGTATTTTC ATTTTAAATA TTAATAAAC CAAGTTTGT TGTAGTTAT	2160
TCTAGCCAAT AAGAAAAGAG AATGTAGCAT CCTAGAGGTG TATTTGTCT GCAGTTTGGC	2220
AGGACCGTCA GTTAGTCCAA ATAAACATCC CCTCAGCGTG GAGGCGAATG GAACCTGTGC	2280
TCCTTTCTTA CGGGAAGCTT TGCAAAGCAA AATAGCAGGG TTACAAGCTT GGAGTTGTTA	2340
AGGCAACTAG AGTTTCTCT ATTAATTTAT AGACTGTTGT TGCACCTACT TAGCTCTTTT	2400
TTGGGAACTC TAGTTCCCAG GGGAAAATAC CTCGTGCC	2438

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 542 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

Ser	Gly	Gly	Gly	Pro	Trp	Arg	Ala	Gly	Gly	Gly	Ser	Gly	Lys	Ser	Asp
1				5						10				15	

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Ser Gly Leu Thr Val Glu Pro Gly Arg Gly Leu Thr Ala Arg Pro Pro	20	25	30
Pro Gly Gly Ser Arg Thr Arg Ser Gly Ser Gly Arg Ala Ser Leu Pro	35	40	45
Arg Leu Ser Glu Arg Arg Val Met Ala Val Val Met Ala Ala Gly Ala	50	55	60
Arg Thr Ala Pro Leu Glu Leu Ser Ser Glu Arg Ser Val Gln Lys Val	65	70	75
Pro Arg Arg Asn Phe Leu Leu Glu Lys Leu Lys Asn Thr Xaa Phe Ile	85	90	95
Thr Leu Glu Ile Val Lys Asn Leu Phe Lys Met Ala Glu Asn Asn Ser	100	105	110
Lys Asn Val Asp Val Arg Pro Lys Thr Ser Arg Ser Arg Ser Ala Asp	115	120	125
Arg Lys Asp Gly Tyr Val Trp Ser Gly Lys Lys Leu Ser Trp Ser Lys	130	135	140
Lys Ser Glu Ser Cys Ser Glu Ser Glu Ala Ile Gly Thr Val Glu Asn	145	150	155
Val Glu Ile Pro Leu Arg Ser Gln Glu Arg Gln Leu Ser Cys Ser Ser	165	170	175
Ile Glu Leu Asp Leu Asp His Ser Cys Gly His Arg Phe Leu Gly Arg	180	185	190
Ser Leu Lys Gln Lys Leu Gln Asp Ala Val Gly Gln Cys Phe Pro Ile	195	200	205
Lys Asn Cys Ser Gly Arg His Ser Pro Gly Leu Pro Ser Lys Arg Lys	210	215	220
Ile His Ile Ser Glu Leu Met Leu Asp Lys Cys Pro Phe Pro Pro Arg	225	230	235
Ser Asp Leu Ala Phe Arg Trp His Phe Ile Lys Arg His Thr Val Pro	245	250	255

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Met Ser Pro Asn Ser Asp Glu Trp Val Ser Ala Asp Leu Ser Glu Arg		
260	265	270
Lys Leu Arg Asp Ala Gln Leu Lys Arg Arg Asn Thr Glu Asp Asp Ile		
275	280	285
Pro Cys Phe Ser His Thr Asn Gly Gln Pro Cys Val Ile Thr Ala Asn		
290	295	300
Ser Ala Ser Cys Thr Gly Gly His Ile Thr Gly Ser Met Met Asn Leu		
305	310	315 320
Val Thr Asn Asn Ser Ile Glu Asp Ser Asp Met Asp Ser Glu Asp Glu		
325	330	335
Ile Ile Thr Leu Cys Thr Ser Ser Arg Lys Arg Asn Lys Pro Arg Trp		
340	345	350
Glu Met Glu Glu Glu Ile Leu Gln Leu Glu Ala Pro Pro Lys Phe His		
355	360	365
Thr Gln Ile Asp Tyr Val His Cys Leu Val Pro Asp Leu Leu Gln Ile		
370	375	380
Ser Asn Asn Pro Cys Tyr Trp Gly Val Met Asp Lys Tyr Ala Ala Glu		
385	390	395 400
Ala Leu Leu Glu Gly Lys Pro Glu Gly Thr Phe Leu Leu Arg Asp Ser		
405	410	415
Ala Gln Glu Asp Tyr Leu Phe Ser Val Ser Phe Arg Arg Tyr Ser Arg		
420	425	430
Ser Leu His Ala Arg Ile Glu Gln Trp Asn His Asn Phe Ser Phe Asp		
435	440	445
Ala His Asp Pro Cys Val Phe His Ser Pro Asp Ile Thr Gly Leu Leu		
450	455	460
Glu His Tyr Lys Asp Pro Ser Ala Cys Met Phe Phe Glu Pro Leu Leu		
465	470	475 480
Ser Thr Pro Leu Ile Arg Thr Phe Pro Phe Ser Leu Gln His Ile Cys		
485	490	495

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Arg Thr Val Ile Cys Asn Cys Thr Thr Tyr Asp Gly Ile Asp Ala Leu  
500 505 510

Pro Ile Pro Ser Pro Met Lys Leu Tyr Leu Lys Glu Tyr His Tyr Lys  
515 520 525

Ser Lys Val Arg Leu Leu Arg Ile Asp Val Pro Glu Gln Gln  
530 535 540

## (2) INFORMATION FOR SEQ ID NO:45:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4999 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

```

CCCTCTGGGC AAGCCGCCCC CCCCCACCC ATCTACCACA CACACACACA CACACACACA      60
CACACATTCA GACCTTGGGG CAAAACAAA GCAAATAAC AACAACAAA AACTGCCTG      120
TGGAAAGTCC TTACTTCAGG AAGGTTGGCA GATGAGGAGC AAGGGAACAT TTTATCAGGA      180
CTGCCACAAA GGAGTCTTTT TTTTAAATGG TTTTCAAGA CAGGGTTTCT CTGTATAGCC      240
CTGGCTGTCC TGGAGCTCAC TTTGTAGACC AGGCTGGCCT CGAACTCAGA AATTGCCTG      300
CCTCTGCCTC CTGAGTGCTG GGATTAAAGG CGTGCAGCAC CATGTCCAAC TGGCATTTC      360
TCAATTAAGG TTCGTCCTT TCAGATAACT CTAGGTTCTG GGTCAAGCTG ACACAAGGCT      420
ACACAGCACA GTTTGTATGC CACATTCAGT TCAGAAGACA CCCAACCTCC CTGGAAGTGG      480
AACTTATGCA CATTTGTGAG CTTCCACTTG GGAGTGGGAA CCTGAAGTGG GTCCTCTCCA      540
AGAGCAGCCG TGCTCTTAAC TGCTGAGCCA TTTCAGCAGC CTCACATCAG AATTAGTTA      600

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GAAATTAGCCG GGTATGAATC ATACCCCTTAG AATCCTAGCA TCTGAAAGCA GAGCTAAGAG  
 660  
 AACACGGCAT TCAAGACCAG CTCTTGGCTA CAGAGCCCGT CCTGTCTTAG GATGGGCTAC 720  
 AAGAGACTAT TTCAAAGCCA TCCAAACAAC AATAACTACA ACAACAACAA GGTAAAAAT 780  
 AGGCTGGGCA CAGGGTACAC ACCTTTAATG CCAACACTCA GGAGGCAGAG CCAGGCTGAT 840  
 CAGTGTGAGT TTGAGTTCAA CGTGGTCTAC ATAGGGAGTT CTAGGCCAGC AGAGCTTACA 900  
 GTCTCTCTCT CTCTCTCTCT CTCTCTCTCT CTCTCACACA CACACACACA CACACACACA 960  
 CACACACACA CACACACGGT GGCATTATGG GATTTTTTTG GGATAAGGTT TCTCTGTCTA 1020  
 GCCCTGGCAT AGATTCACTC TGTAGACTAG GCTAGCCCTG AACTCAGAGA TCCGCCTGCC 1080  
 TCTGCCTCCC AAGTGCTGGG ATTATAGGTG TTGCACCACC ACTGCCCAGC CACTTTGGGA 1140  
 TTTTGAAGT GTTATCAAGA GGCTTTGAG GAGGTCAAAC TTCAACAGCA ACCTCTCCAT 1200  
 GATAATGTAG CTAATGATCA AACGACACTC AAAACTTAAC CCTTAAAGCA CACATCCACC 1260  
 AGACAGCGTG CCCACTCGTA GTTCCATTAC TCAGGAGGCT GAAGCAGGAG GATGAAGGAC 1320  
 TAAGGCTTCA GCAACCTAGG GAGCCGCAGG GGACAGTAGT CTCAATCCCT ACATTCTCCT 1380  
 GAACACAGGA GCAGGAGTTC AGGAAGGGTG TCAAGGCCGC TTAGTGATCT TAGGGCCTCA 1440  
 GGAATGACTA GCTCAGGCAG AGAGAGCAAA GGTCTCCAGT GGAGAAGTCT ACACACACAC 1500  
 ACACACACAC ACACACACAC ACACACACAC AGAATCCAAG GCGATGACGT CATCAAAGGG 1560  
 TTAATTCTAG TCTGGGATGG GGGGGAGGGT GGGGCACGCA GCTGTCAGGT GGCTTTGGAA 1620  
 AAATAAACTG CTGAAGAGTC TGACGCCAGG GAGTCTGGG AGGGACAAGA GGTACCCAC 1680  
 TCAAAGAGTG TGCTCCACAA ACCATGCCCG CTGTCTCACG TCTGGAGTCG TCACTTATTT 1740  
 TTTGCCCTGA TTCTTTGTAG CCGGTGGGT CTCAAGGCCG TAAGTGCTGT GCGCGCCGTG 1800  
 GTCTGGGAGG TGACGATAGG GTTAATCGTC CACAGAGCCC AGGGCCGGAG CCGCGCCGGG 1860  
 CGTCCGCAGC CCGGCTGGAG CCGGAAGCAG TGGCTGGTCA GGGCCGCTTC TAGCCTTCCC 1920

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TATCTGTACT	TCCACAGAGG	TCTCTGCGAG	CTAGGGGGAC	AGTGAGGTGC	GGGGTAGGGG	1980
CCCGGGCTTA	GAGCCAGCAA	GGGGACGGTT	CACGGTAAGG	TCTGAGGGAG	AGAGAGCTCC	2040
TGAGAAACTT	GGGGGGCGCG	ACACAGATAG	GGTGAAAGCA	GAGTGATAGA	CCTGGGATGG	2100
TTAGGGGACC	AAGGGAAGAC	CAGGCTGGTT	GGCATAACCC	GGTGAACGGA	TGGGAGTCCT	2160
AAGGAAAGAT	GATGCGCCTA	ACAGTCCTTT	CTGTCTCCAC	ACCACTCCAG	GGGACGATCC	2220
GGAGCTCAAC	TTTCAAAAGC	GAGACGCCCC	AGCAAGCCTG	TTTGAAGAAG	TTCTTCAGCG	2280
GCTCTCCTCA	TGGGCCAGAC	GGCCCTGGCA	AGGGGCAGCA	GCAGCACCCC	TACCTCGCAG	2340
GCTCTGTACT	CGGACTTCTC	TCCTCCCGAG	GGCTTGGAGG	AGCTCCTGTC	TGCTCCCCCT	2400
CCTGACCTGG	TTGCCCAACG	GCACCACGGC	TGGAACCCCA	AGGATTGCTC	CGAGAACATC	2460
GATGTCAAGG	AAGGGGGTCT	GTGCTTTGAG	CGGGCCCCTG	TGGCCCAGAG	CACTGATGGA	2520
GTCCGGGGGA	AACGGGGCTA	TTGAGAGGTT	CTGCACGGCT	GGGAGATCAG	CTGGCCCCTG	2580
GAGCAAAGGG	GCACACACGC	CGTGGTGGGC	GTGGCCACCG	CCCTCGCCCC	GCTGCAGGCT	2640
GACCACTATG	CGGGCGTTTT	GGGCAGCAAC	AGCGAGTCCT	GGGGCTGGGA	TATTGGGCGG	2700
GGAAATTTGT	ATCATCAGAG	TAAGGGCCTC	GAGGCCCCCC	AGTATCCAGC	TGGACCTCAG	2760
GGTGAGCAGC	TAGTGGTGCC	AGAGAGACTG	CTGGTGGTTC	TGGACATGGA	GGAGGGGACT	2820
CTTGGCTACT	CTATTGGGGG	CACGTACCTG	GGACCAGCCT	TCCGTGGACT	GAAGGGGAGG	2880
ACCCCTATATC	CCTCTGTAAG	TGCTGTTTGG	GGCCAGTGCC	AGGTCCGCAT	CCGCTACATG	2940
GGCGAAAGAA	GAGGTGAGAT	ACGGACTAGG	TGTGGGGAGA	TCACTACTCT	TGGCAATGGT	3000
TTGGGCTGGA	AACTCATGGT	TGGAGCACAG	GAAGTAGGCT	TCTTGTCACT	TTGGCCTGTC	3060
ACTTAGATGG	CCTTGGATCT	AGCTTCACTC	CCAATCCCTA	TTGGATGTGA	TGCACAAATT	3120
CAGAGCCTTT	GGGTCTCCCT	CAGCTGAGGT	GGCGTGGGAA	ATGGAGGAAG	AAGGAAGGGT	3180
GCCTGAGCAG	GATCTCAAGT	TCAAGGATGC	CTGGAGTTGC	TTACTTACCT	TGTCTTCCTT	3240
CTCTCTCCGC	AGTGGAGGAA	CCACAATCCC	TTCTGCACCT	GAGCCGCCCTG	TGTGTGGGCC	3300

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ATGCTCTGGG GGACACCCCG CTGGGTCAAA TATCCACTCT GCCTTTGCCC CCTGCCATGA	3360
AGCGCTATCT GCTCTACAAA TGACCCAGTA GTACAGGGTG TGCTGGCACC CTACCGTGGG	3420
GACAGGTGGA GAGGCACCCG CTGGCCTAGA CAACTTTAAA AAGCTGGTGA AGCTGGGGGG	3480
GGGGGCTGG ACCCCTTCAC CTCCCCTCT CACAGGAGCA AGACATATAG AAATGATATT	3540
AAACACCATG GCAGCCTGGG ACAAAGAGGT TTTTGAAGTA AAAAATGAGA TGTATTGTCA	3600
CAACCTGTTT CATATTGTT TTTCTTTTG TTTTACACTC CCCCACCCCA GGCTAGAGCC	3660
CCATCACTGT CTTAAGGAAT TATGACAACC CACAAAGCTC AGGCCCAGGT GTTTATTTCC	3720
CTTACATGTA GGATGTTCA CAAACACAAT ACAGGGGCTT TGGCACCGTG GGGGAGGGGA	3780
CTATCCCAGG CCTCTTAGGG TCTCATGTAT ACCGAATTCA GACCCGAAAG CTCTGAATTT	3840
CTGCATCAGA CATCCAGTAG AACTTGGGAG TGAAGCTAGA GCCAAGGCCA TCTAASTGAC	3900
AGGCCAAAGT GACACGAAGC CCACTTCCTG TGCTCCAACC ATGAGTTTCC AGCCCAAACC	3960
AATGGAAGGT GATTTCACTT GTCAGGGCCC AAAGGGACAG TCAGTTCTAC TCCCTCCCTT	4020
CACTAGGAGC CACCTTGGTG ACAGTTGATT CTACCCACTG TAAGTGGTAA AGGGATTGGC	4080
CTGGTCCCAA CCATAATAGG GCGGTGGAAA CGGCTCAGGA GGGTACAGCG TGGATTAGGC	4140
CACAAGATGG GGCAGATGAT GTCATCAGAA GCATGTGACC GGTGGGAGCA GTTACTAAAC	4200
TTCTGGGCAG CCTAGTCCAT GCTATGCAGG CAGGTAGAGG GATGGGCAGT GCTCATTTGT	4260
TGGCATTGAT GATGTCCACA AATTCAGGCT TGAGAGATGC GCCACCCACA AGGAAGCCGT	4320
CCACGTCAGG CTGGCTTGCC AGCTCTTGC AGGTTGCTCC AGTCACAGAA CCTGTACCAG	4380
GAACAAGAAG ACAGTTTGGT CAGGTCTATG ATCAGAACAC TTAAGCCCCA CCTCTCTGTG	4440
CAAGGCAGCC TCAGTCTGTC TTAGCCCAAT TCCGTCTTAG CTAGAGCCAA AGCCACTCAC	4500
CTOCATAAAT GATCCGGGTG CTCTGAGCCA CCCCATCATT GACATTGGAT TTCAGCCATC	4560
CCCCGAGCTT CTCGTGTACT TCCTGTGCCT AGAAGGAGGA GGCAGAGCTA CTAAGTAAGC	4620
TCCTTCCTAT CTATCATTCA AGGAGTAAAA ACCACTGGTT CTCACATAGA GTTGAGTTTC	4680

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CAGAAAAGCC CCGGGACCAG AGAGTGGCAA GGCTCCAATC CCACCAGGCT TGGGAATGAAC 4740  
 ATTTTGGCA AAGTCACTCT CCTTGGTGAG TTTGGGGGCC CTCTGTCTCT AAAGGGGCTT 4800  
 GGATGGGCTC CATAGCTGTG TGAGTCTGTT AAAGCCGGAC AGGCTGAGGA GCTCTGGGTA 4860  
 GTTACCTGCT GAGGGGTTGC CTTCTTGCCA GTCCCAATGG CCCACACAGG TTCATAGGCC 4920  
 AGGACCACCT TGCTCCAGTC TTTCACATTA TCTGTGGGGC AGAGAGGAGA GTGAGTAGGA 4980  
 AGGAGCTGAC CCGCCAAGC 4999

## (2) INFORMATION FOR SEQ ID NO:46:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 264 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

Met	Gly	Gln	Thr	Ala	Leu	Ala	Arg	Gly	Ser	Ser	Ser	Thr	Pro	Thr	Ser
1					5				10					15	
Gln	Ala	Leu	Tyr	Ser	Asp	Phe	Ser	Pro	Pro	Glu	Gly	Leu	Glu	Glu	Leu
			20					25					30		
Leu	Ser	Ala	Pro	Pro	Pro	Asp	Leu	Val	Ala	Gln	Arg	His	His	Gly	Trp
			35				40				45				
Asn	Pro	Lys	Asp	Cys	Ser	Glu	Asn	Ile	Asp	Val	Lys	Glu	Gly	Gly	Leu
		50				55					60				
Cys	Phe	Glu	Arg	Arg	Pro	Val	Ala	Gln	Ser	Thr	Asp	Gly	Val	Arg	Gly
65					70					75				80	
Lys	Arg	Gly	Tyr	Ser	Arg	Gly	Leu	His	Ala	Trp	Glu	Ile	Ser	Trp	Pro
			85				90						95		
Leu	Glu	Gln	Arg	Gly	Thr	His	Ala	Val	Val	Gly	Val	Ala	Thr	Ala	Leu

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100	105	110
Ala Pro Leu Gln Ala Asp His Tyr Ala Ala Leu Leu Gly Ser Asn Ser		
115	120	125
Glu Ser Trp Gly Trp Asp Ile Gly Arg Gly Lys Leu Tyr His Gln Ser		
130	135	140
Lys Gly Leu Glu Ala Pro Gln Tyr Pro Ala Gly Pro Gln Gly Glu Gln		
145	150	155
Leu Val Val Pro Glu Arg Leu Leu Val Val Leu Asp Met Glu Glu Gly		
165	170	175
Thr Leu Gly Tyr Ser Ile Gly Gly Thr Tyr Leu Gly Pro Ala Phe Arg		
180	185	190
Gly Leu Lys Gly Arg Thr Leu Tyr Pro Ser Val Ser Ala Val Trp Gly		
195	200	205
Gln Cys Gln Val Arg Ile Arg Tyr Met Gly Glu Arg Arg Val Glu Glu		
210	215	220
Pro Gln Ser Leu Leu His Leu Ser Arg Leu Cys Val Arg His Ala Leu		
225	230	235
Gly Asp Thr Arg Leu Gly Gln Ile Ser Thr Leu Pro Leu Pro Pro Ala		
245	250	255
Met Lys Arg Tyr Leu Leu Tyr Lys		
260		

## (2) INFORMATION FOR SEQ ID NO:47:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5615 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

GTACTTTCTT TATATCTCCA TAATTTTATT TACTATTACT ACATGATACA TTATTTTATA	60
AAAGTCTTTG TAACCTCCTT AAGGATTCAC TGCTTAATCT CCAGTGCTTA GCACAAATCA	120
TTAAATGCGA ACCAGAAACT CTCCTAAATG TGTACATCT ATAACCTCAT TGGATTCTCA	180
CTACCAACCC CATGCAATAG ATACTAATGT GATCTCTGTC TTACAGAGGA AGAAACAGGC	240
ACAGGGAGGT TCAGTAATTT GCCCAAGGTC ATACACACAC TGGCCTTCAG GTATTCATGC	300
CCGGGGAGTC TGGTCCACA GCTGGCATGT TTGCCATTAT ATTATATTGC CTCCTTATAG	360
TGTCGGCACT CATTAAGCAC ATGACAGCT ATGCTTGGTG AGTGACTACT ATGTACCCAG	420
CTCTGTGCTA CATGCTTTAC CTGGATTATT TCAACTGCAC AACAAACCTG TGAGGTAACT	480
ACCATCATTG CTCTATTTT ACATAACAGA AACTACAGA AATCTGGGGC TGGGCGTAGT	540
GGCTCATGCC TGAAATCCCA GCACTTTGGG AGACCTGTC TCTAAAAAA ATTTTTTTTT	600
GGCCGGACGT GGTGGCTCAC ACCTGTAATC TCAGCACTTT GGGAGGCTAA GGCAGGCAGA	660
TCACAAGGTC AGGAGTTCTA GACCAGCCTG GCCAACATGG CAAAACCTG TGTCTACTAA	720
AAATACAAA AATAGCTAGG CGTGGTGGCA GGTGCTGTA ATCCCAGCTA CTCAGGAGGC	780
TGAGGCAGGA GAATCCCTG AACCTGGGAG ATGGAGGTTA CAGAGAGCCG AGATGCTGCC	840
GCTGCACTCC AGCCTGGGCA ACAAGAGCAA GACTCTGTCT CGAAAAAAT AAAAATAAAA	900
ATAAAAATAT TTTTTTAAA ATTAGCTGGG TGTGGTAGCA CATGCTGTA GTCCAGCTA	960
CTTGGGAGGC TGAGGTAGGA GGATCACTTG AGCCAGGAG GTCAAGGCTG CAGTGGGCTG	1020
TGATGGCGCC ACTGCACTCT AGCCTTGGTG ACAGCAAGAC CCGTCTCAA AAAAAAAAAA	1080
AAGAGAAATC GGGCAACTTC CCCAAGATCG CGCAATTAAC TAGTGGCATA GCTTCACTCA	1140
AACTCGAAGT CTTAATCAGG AACTCTACC AAATGAGATC AACGGCTCAG TAATGGATTG	1200
GCATCCAGTA TGAAGACTGG ACCAGCAGGG AGAACTATGA TCGGTACAGC CTAGAGCCTG	1260
AAGCAGATTT CACAGCCTCA GAGGTGGCAC AGGCTGACTC ACAACCCGGG GCAGAAAGGG	1320

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ACCAGCCACG AAACAGTGAC CCAGAATCAC AGGGAAGTAG AAATGGGATT CGGCACAATG	1380
AAGCCCCCTCC TTGACCCCAT GCTCCTTACC CTCAGGGGCG CAGGAGTTAG TCGCTCAGGC	1440
GGCTCAAAGG TCTTGACGGT GGAGAACACC ATCCCCAGGG ATTCCCGACG CGGTGATGCC	1500
ATCAAAGCGT TAATTCTGAG ATGGGCCTGC CCGGTPCGG ACTCTGCCGC AGCAAGAGAA	1560
GGGTFAACTG CCCCCGGCCT TCGCCGTGGG GCGGGGGCCT CGGGGAGGGT CACAGCCCCG	1620
GACTGAGACC CGAGGTTAAC CGCCCCGGGT GGGCTCCAG GGGGCGGGC ATGCTCTCCG	1680
CGGCTGCTGC CGGTATAGAG CGGTAAGTGC CCAGGAGGGG GCGGGGCCCC ACAGGGGCGT	1740
GGCCTCCGAG CTGCACGGCC GTGGGCGGGG ATGAGAGGGT TAAGCCCCAG AGGGCCCTGG	1800
AGGGGCGGGG CCGCGGGACG GGCTCGGCCC AAGGGAGGAG CTGGGGGCGG AAGCGGCGG	1860
CGGTCTGCCG CCTGCGCGCC TCGGCTTCTT TCGGCCCCG TCCTTCAGAG GCGCGCGAC	1920
CTCCAGGGCT GGAAGTCAA CCGAGGTTG GGGGACGGG CGAGGGCTCC GGGCGAGTAA	1980
GGGGATGGT CCATGCTGAG GCCCAAATGG GCGGAAGTGC CGAGAGTCTC TGGCGACCTG	2040
GATCAGATGG GCGGAGGGCA GATGAAGGGC CCAGGAGCTT TGGGGCAGCG AGGAGGGAGG	2100
AGCGGGCCCC TTGGCAAACT TGGGTGAAAG GATGGGGTAC CTGGGTGACG AGCCCCCCCC	2160
AGGATTCTGC TCTTCACGCC CCTTTCTCTC CAGCTCCCTT CCAGGTCAAT CCAAAGTGA	2220
GCTCAACTTT CAGAAGAGAA AGACGCCCCA GCAAGCCTCT TCGGGGAGT CCTCTAGCTC	2280
CTCACCTCCA TGGGCCAGAC AGCTCTGGCA GGGGGCAGCA GCAGCACCCC CACGCCACAG	2340
GCCCTGTACC CTGACCTCTC CTGTCCCGAG GGCTTGAAG AGCTGCTGTC TGCACCCCCCT	2400
CCTGACCTGG GGGCCCAGCG GCGCCACGGT TGGAAACCCA AAGACTGTTC AGAGAACATC	2460
GAGGTCAAGG AAGGAGGGTT GTACTTTGAG CGGCGGCCCC TGGCCCAGAG CACTGATGGG	2520
CCCCGGGGTA AGAGGGGGTA TTCAAGGGGC CTGCACGCCT GGGAGATCAG CTGGCCCCCTA	2580
GAGCAGAGGG GCACGCATGC CGTGGTGGGC GTRGCCACGG CCTCGCCCC GCTGCAGACT	2640
GACCACTACG CGCGCTGCT GGCAGCAAC AGCGAGTCGT GGGGCTGGGA CATCGGGCGG	2700

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GGGAAGCTGT ACCATCAGAG CAAGGGGCCC GGAGCCCCC AGTATCCAGC GGGAACTCAG	2760
GGTGAGCAGC TGGAGGTGCC AGAGAGACTG CTGGTGGTTC TGGACATGGA GGAGGGAACT	2820
CTGGGCTACG CTATTGGGGG CACCTACCTG GGGCCAGCAT TCCGCGGACT GAAGGGCAGG	2880
ACCCTCTATC CGGCAGTAAG CGGTGTCTGG GGCCAGTGCC AGGTCCGCAT CCGCTACCTG	2940
GGCGAAAGGA GAGGTGAGGC CTGGGGCAGA CGTGGGGAGA ACTTCTGTG CCTGGTGGCA	3000
GTGCTTTGGG ATGGAAACTC TTCTGACAAG AGCAGAGGGG ATGGACCTTC ATCCAGCCTG	3060
CCTCAACCTC TGTTCAGTGC TGGGAAAGGC TAGGGGTCTT CACAGCTGTT ATTTAATTTA	3120
ACCCAACAGC AATAGAGGTG AAACAGGCTT GAGAAAGCAA CTTTCTCAAG TTCTCTTGGC	3180
CAGTAAATGG TGAACCTTCA GAATGGAGGG AGGAACTGCA GGGATGAGAG AATTCAGGAG	3240
ATATCAACCC CTGAGCAAGA GTGCCAAGC GTTAGGTACT GGGTTTGATG TACAGCTCCA	3300
AAAGAAGGAT GGGCAGAGCC AGGTACCCAG GCTGTATACC GGATTCCCTG GGCTCTAACC	3360
TGTCTCTGTG CCACATACCT ACTTCCTTCC TCAGCCACAC CTCTGGATGG AGACACTGGG	3420
GCCCTGGGCA CCAGGGAGGA GAGCAGTGGG GGAGGCAGGG CCTTAGGGTG GGGCAACAGG	3480
GGAGGAGCCT CCCCAGGAAC TGA CTGGGTC CAGGGCTTGG AGCTGCTCTC TGCAGTTGTG	3540
TGGGCTGTAG AGTGGAGGGC CATCCCTCCT CACCTCAGCC CCAGCTCCCA AGCCTCTGGA	3600
GTCAAAGCCT GGGCCAGCTC CACCACTGTC AGAGCCACCT TGGCCTGTTG TTTAGAGGGC	3660
CTTAGCCAGC TCTTCACCCC CAGCTCTGAC TAGGGATGTG TGAAATCTTA TCTGGGAGCC	3720
AGAACTTCCG GGTATCTCAA ATTCCCCTTT CAGCCAGGTG GGCACACTCG AAGCAGGAAA	3780
GCAGAAAGGC ATCTGAGTAG GACCCCGTAG TTTGAGGACA TCTGGCTGGT GGCTGCACCC	3840
ATACTTACAT TCCCCTCCTT CTCTCTCCCA GCGGAGCCAC ACTCCCTTCT GCACCTGAGC	3900
CGCCTGTGTG TGGGCCACAA CCTGGGGGAT ACCCGGCTCG GCCAGGTGTC TGCCCTGCCC	3960
TTGCCCCCTG CCATGAAGCG CTACCTGCTC TACCAGTGAG CCCTGTGATA CCACAGACTG	4020
TGCTGAGGTC TTGCCACCAC CCCTCCCCTT GGGGAGGTGG GGAGGCACTG CTGGCCTAGA	4080



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CCAGCTGCTG AAAGCTGGTG AGGCTGAGCC CCTACCCCAA CCCAAGCTCT GCGGAAATCA	4140
ACAGCCCCAG AGCCACTTGG AGGGAGGAAG AAAGGGAGCC GCGTTCAAG GCTATGACAG	4200
TCTGCTACGC AAAACATTTT TTCAAGTAAA AATAGTAAGA GATGTTGTTA TAGAAACCTG	4260
TTCTTGTTFP TTTTTTTTTC TTGCACAAAT GATCATTTAT ATAGCTGCCT CAAAAAGGAA	4320
GATTATCTGG GCAAGTCCAG TGAAGGCAGA CAAACCACAA GACCTAGTGC CAGGTTTATT	4380
CCCTCACATG GGTGGTTTAC ATACACAGCA CAGAGGCACG GGCACCATGG GAGAGGGCAG	4440
CACTCCTGCC TTCTGAGGGG ATCTTGGCCT CACGGTGTA GAAGGGAGAG GATGGTTTCT	4500
CTTCTGCCCC CACTAGGGCC TAGGGAACCC AGGAGCAAAT CCCACCACGC CTTCCATCTC	4560
TCAGCCAAGC AGAAGCCACC TTGGTGACGT TTAGTTCCAA CCATTATAGT AAGTGGAGAA	4620
GGGATPGGCC TGGTCCCAAC CATTACAGGG TGAAGTATA AACAGTAAAG GAAGATACAG	4680
TTTGGATGAG GCCACAGGAA GGAGCAGATG ACACCATCAG AAGCATATGC AGGGAAAGGG	4740
CAGTTACTGG GCTTCTGGGC TGCTTAGTCC CTGGCTTGGC AGGAAGGCTA GGAAGATGG	4800
ATGGGGCTCA TTGTTTGGCA TTGATGATGT CCACGAATTC GGGCTTGAGG GAAGCACCAC	4860
CCACAAGGAA GCCATCCACA TCAGGCTGGC TGGCCAGCTC CTTGCAGGTT GCCCCAGTCA	4920
CAGAGCCTGG GAAGGGAGCA GAACAAGGGC TTGGTCAAGA ATGGGATGAG TCTGCCCCAT	4980
CCCCACCTCC ATGTCCGAGG GCTCAGTCTA GTCTCAGCC CACTCCACCT CAGCCGGGAA	5040
CCAAAGCCAC TCACCTCCAT AAATGATACG GGTGCTCTGA GCCACCCCAT CAGAGACGTT	5100
GGACTTCAGC CATCCTCGGA GCTTCTCGTG TACTTCCTGG GCCTAGAACA AGAAGCTGGC	5160
CTAAGTAAGA CCTTTCTGTC CTCTCTAAGA GGAAAAATCA CTGGCACCAG TGGACACTTA	5220
GTGTGGTTTC TGA CTGAGTACAG GGCTCTGATC CAAGCCAGGC CCTGGACTGG	5280
ATGCCCTTGG ACAAGTCACT GTCTCTGGGT TCAAGGTCTC TGTGTCTTTG AAATAAGGGG	5340
TTGCCCCATG TGGGCTGTGT CTGTCCAAAC CTATTGAGGC AGGCTGGGAT GAGGGCAGGG	5400
CTCCTGGGCC CGGTTACCTG TTGGGGTGTT GCAGTCTTGC CAGTACCAAT GGGCCACACA	5460

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GGCTCATAGG CCAGGACGAC CTGCTCCAG TCCTTCACGT TATCTGCAGG GCAGAGATAC 5520  
 AGATGGAGGG AAGGGTGAAC AAGAAAGAGC TCTCCAGCCA GGTCTCCGG AGTACGAAGA 5580  
 ACGGTGGCCT ACTGCCCCCT AGTGGACATT GGGGG 5615

## (2) INFORMATION FOR SEQ ID NO:48:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 263 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

Met	Gly	Gln	Thr	Ala	Leu	Ala	Gly	Gly	Ser	Ser	Ser	Thr	Pro	Thr	Pro	1	5	10	15
Gln	Ala	Leu	Tyr	Pro	Asp	Leu	Ser	Cys	Pro	Glu	Gly	Leu	Glu	Glu	Leu	20	25	30	
Leu	Ser	Ala	Pro	Pro	Pro	Asp	Leu	Gly	Ala	Gln	Arg	Arg	His	Gly	Trp	35	40	45	
Asn	Pro	Lys	Asp	Cys	Ser	Glu	Asn	Ile	Glu	Val	Lys	Glu	Gly	Gly	Leu	50	55	60	
Tyr	Phe	Glu	Arg	Arg	Pro	Val	Ala	Gln	Ser	Thr	Asp	Gly	Ala	Arg	Gly	65	70	75	80
Lys	Arg	Gly	Tyr	Ser	Arg	Gly	Leu	His	Ala	Trp	Glu	Ile	Ser	Trp	Pro	85	90	95	
Leu	Glu	Gln	Arg	Gly	Thr	His	Ala	Val	Val	Gly	Val	Ala	Thr	Ala	Leu	100	105	110	
Ala	Pro	Leu	Gln	Thr	Asp	His	Tyr	Ala	Ala	Leu	Leu	Gly	Ser	Asn	Ser	115	120	125	

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Glu Ser Trp Gly Trp Asp Ile Gly Arg Gly Lys Leu Tyr His Gln Ser  
 130 135 140  
 Lys Gly Pro Gly Ala Pro Gln Tyr Pro Ala Gly Thr Gln Gly Glu Gln  
 145 150 155 160  
 Leu Glu Val Pro Glu Arg Leu Leu Val Val Leu Asp Met Glu Glu Gly  
 165 170 175  
 Thr Leu Gly Tyr Ala Ile Gly Gly Thr Tyr Leu Gly Pro Ala Phe Arg  
 180 185 190  
 Gly Leu Lys Gly Arg Thr Leu Tyr Pro Ala Val Ser Ala Val Trp Gly  
 195 200 205  
 Gln Cys Gln Val Arg Ile Arg Tyr Leu Gly Glu Arg Arg Ala Glu Pro  
 210 215 220  
 His Ser Leu Leu His Leu Ser Arg Leu Cys Val Arg His Asn Leu Gly  
 225 230 235 240  
 Asp Thr Arg Leu Gly Gln Val Ser Ala Leu Pro Leu Pro Pro Ala Met  
 245 250 255  
 Lys Arg Tyr Leu Leu Tyr Gln  
 260

## (2) INFORMATION FOR SEQ ID NO:49:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

AGCTAGATCTGGACCTACAATGGCAGC

28

## (2) INFORMATION FOR SEQ ID NO:50:

## (i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

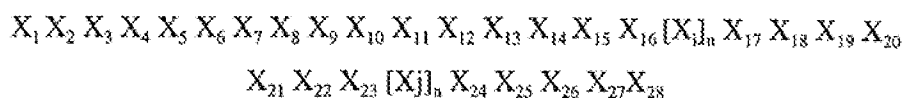
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

AGCTAGATCT GCCATCCTAC TCGAGGGGCC AGCTGG

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## CLAIMS:

1. A nucleic acid molecule comprising a sequence of nucleotides encoding or complementary to a sequence encoding a protein or a derivative, homologue, analogue or mimetic thereof or a nucleotide sequence capable of hybridizing thereto under low stringency conditions at 42°C wherein said protein comprises a SOCS box in its C-terminal region.
2. A nucleic acid molecule according to claim 1 wherein the protein further comprises a protein:molecule interacting region.
3. A nucleic acid molecule according to claim 1 wherein the protein:molecule interacting region is located in a region N-terminal of the SOCS box.
4. A nucleic acid molecule according to claim 2 or 3 wherein the protein:molecule interacting region is a protein:DNA binding region or a protein:protein binding region.
5. A nucleic acid molecule according to claim 4 wherein the protein:molecule interacting region is one or more of an SH2 domain, WD-40 repeats or ankyrin repeats.
6. A nucleic acid molecule according to any one of claims 1-5 wherein the SOCS box comprises the amino acid sequence:



wherein:  $X_1$  is L, I, V, M, A or P;  
 $X_2$  is any amino acid residue;  
 $X_3$  is P, T or S;  
 $X_4$  is L, I, V, M, A or P;  
 $X_5$  is any amino acid;  
 $X_6$  is any amino acid;

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$X_7$  is L, I, V, M, A, F, Y or W;

$X_8$  is C, T or S;

$X_9$  is R, K or H;

$X_{10}$  is any amino acid;

$X_{11}$  is any amino acid;

$X_{12}$  is L, I, V, M, A or P;

$X_{13}$  is any amino acid;

$X_{14}$  is any amino acid;

$X_{15}$  is any amino acid;

$X_{16}$  is L, I, V, M, A, P, G, C, T or S;

$[X]_n$  is a sequence of n amino acids wherein n is from 1 to 50 amino acids and wherein the sequence  $X_i$  may comprise the same or different amino acids selected from any amino acid residue;

$X_{17}$  is L, I, V, M, A or P;

$X_{18}$  is any amino acid;

$X_{19}$  is any amino acid;

$X_{20}$  L, I, V, M, A or P;

$X_{21}$  is P;

$X_{22}$  is L, I, V, M, A, P or G;

$X_{23}$  is P or N;

$[X]_n$  is a sequence of n amino acids wherein n is from 1 to 50 amino acids and wherein the sequence  $X_j$  may comprise the same or different amino acids selected from any amino acid residue;

$X_{24}$  is L, I, V, M, A or P;

$X_{25}$  is any amino acid;

$X_{26}$  is any amino acid;

$X_{27}$  is Y or F; and

$X_{28}$  is L, I, V, M, A or P.

7. A nucleic acid molecule according to claim 6 wherein the protein modulates signal transduction.

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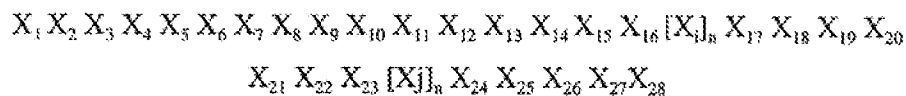
8. A nucleic acid molecule according to claim 7 wherein the signal transduction is modulated by a cytokine or a hormone, a microbe or a microbial product, a parasite, an antigen or other effector molecule.
9. A nucleic acid molecule according to claim 8 wherein the protein modulates cytokine-mediated signal transduction.
10. A nucleic acid molecule according to claim 9 wherein the signal transduction is mediated by one or more of the cytokines EPO, TPO, G-CSF, GM-CSF, IL-3, IL-2, IL-4, IL-7, IL-13, IL-6, LIF, IL-12, IFN $\gamma$ , TNF $\alpha$ , IL-1 and/or M-CSF.
11. A nucleic acid molecule according to claim 10 wherein the signal transduction is mediated by one or more of IL-6, LIF, OSM, IFN- $\gamma$  and/or thrombopoietin.
12. A nucleic acid molecule according to claim 11 wherein the signal transduction is mediated by IL-6.
13. A nucleic acid molecule according to claim 1 wherein the nucleotide sequence encodes an amino acid sequence substantially as set forth in SEQ ID NO. 4, SEQ ID NO. 6, SEQ ID NO. 8, SEQ ID NO. 10, SEQ ID NO. 12, SEQ ID NO. 14, SEQ ID NO. 18, SEQ ID NO. 21, SEQ ID NO. 25, SEQ ID NO. 29, SEQ ID NO. 36, SEQ ID NO. 41, SEQ ID NO. 44, SEQ ID NO. 46 or SEQ ID NO. 48 or an amino acid sequence having at least about 15% similarity to all or part of the listed sequences or a nucleotide sequence which hybridizes to the nucleic acid molecule under low stringency conditions at 42°C.
14. A nucleic acid molecule according to claim 1 wherein the nucleotide sequence is substantially as set forth in SEQ ID NO. 3, SEQ ID NO. 5, SEQ ID NO. 7, SEQ ID NO. 9, SEQ ID NO. 11, SEQ ID NO. 13, SEQ ID NO. 15, SEQ ID NO. 16, SEQ ID NO. 17, SEQ ID NO. 20, SEQ ID NO. 22, SEQ ID NO. 23, SEQ ID NO. 24, SEQ ID NO. 26, SEQ ID NO. 27, SEQ ID NO. 28, SEQ ID NO. 30, SEQ ID NO. 31, SEQ ID NO. 32, SEQ ID NO. 33, SEQ ID NO. 34, SEQ ID NO. 35, SEQ ID NO. 37, SEQ ID NO. 38, SEQ ID NO. 39, SEQ ID NO. 40, SEQ

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ID NO. 42, SEQ ID NO. 43, SEQ ID NO. 45 or SEQ ID NO. 47 or a nucleotide sequence having at least 15% similarity to all or a part of the listed sequences or a nucleotide sequence capable of hybridizing to the listed sequences under low stringency conditions at 42°C.

15. A nucleic acid molecule comprising a sequence of nucleotides encoding or complementary to a sequence encoding a protein or a derivative, homologue, analogue or mimetic thereof or a nucleotide sequence capable of hybridizing thereto under low stringency conditions at 42°C wherein said protein exhibits the following characteristics:

- (i) comprises a SOCS box in its C-terminal region wherein said SOCS box comprises the amino acid sequence:



- wherein:
- $X_1$  is L, I, V, M, A or P;
  - $X_2$  is any amino acid residue;
  - $X_3$  is P, T or S;
  - $X_4$  is L, I, V, M, A or P;
  - $X_5$  is any amino acid;
  - $X_6$  is any amino acid;
  - $X_7$  is L, I, V, M, A, F, Y or W;
  - $X_8$  is C, T or S;
  - $X_9$  is R, K or H;
  - $X_{10}$  is any amino acid;
  - $X_{11}$  is any amino acid;
  - $X_{12}$  is L, I, V, M, A or P;
  - $X_{13}$  is any amino acid;
  - $X_{14}$  is any amino acid;
  - $X_{15}$  is any amino acid;
  - $X_{16}$  is L, I, V, M, A, P, G, C, T or S;



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$[X]_n$  is a sequence of  $n$  amino acids wherein  $n$  is from 1 to 50 amino acids and wherein the sequence  $X_i$  may comprise the same or different amino acids selected from any amino acid residue;

$X_{17}$  is L, I, V, M, A or P;

$X_{18}$  is any amino acid;

$X_{19}$  is any amino acid;

$X_{20}$  L, I, V, M, A or P;

$X_{21}$  is P;

$X_{22}$  is L, I, V, M, A, P or G;

$X_{23}$  is P or N;

$[X]_n$  is a sequence of  $n$  amino acids wherein  $n$  is from 1 to 50 amino acids and wherein the sequence  $X_j$  may comprise the same or different amino acids selected from any amino acid residue;

$X_{24}$  is L, I, V, M, A or P;

$X_{25}$  is any amino acid;

$X_{26}$  is any amino acid;

$X_{27}$  is Y or F;

$X_{28}$  is L, I, V, M, A or P; and

- (ii) comprises at least one of an SH2 domain, WD-40 repeats and/or ankyrin repeats or other protein:molecule interacting domain in a region N-terminal of the SOCS box; and
- (iii) modulates signal transduction.

16. An isolated protein or a derivative, homologue or mimetic thereof comprising a SOCS box in its C-terminal region.
17. An isolated protein according to claim 16 wherein the protein further comprises a protein:molecule interacting region.
18. An isolated protein according to claim 17 wherein the protein:molecule interacting region

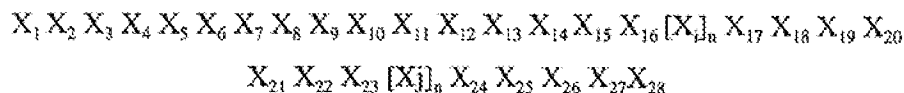
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is located in a region N-terminal of the SOCS box.

19. An isolated protein according to claim 16 or 17 wherein the protein:molecule interacting region is a protein:DNA binding region or a protein:protein binding region.

20. An isolated protein according to claim 19 wherein the protein:molecule interacting region is one or more of an SH2 domain, WD-40 repeats or ankyrin repeats.

21. An isolated protein according to any one of claims 16-20 wherein the SOCS box comprises the amino acid sequence:



wherein:

- $X_1$  is L, I, V, M, A or P;
- $X_2$  is any amino acid residue;
- $X_3$  is P, T or S;
- $X_4$  is L, I, V, M, A or P;
- $X_5$  is any amino acid;
- $X_6$  is any amino acid;
- $X_7$  is L, I, V, M, A, F, Y or W;
- $X_8$  is C, T or S;
- $X_9$  is R, K or H;
- $X_{10}$  is any amino acid;
- $X_{11}$  is any amino acid;
- $X_{12}$  is L, I, V, M, A or P;
- $X_{13}$  is any amino acid;
- $X_{14}$  is any amino acid;
- $X_{15}$  is any amino acid;
- $X_{16}$  is L, I, V, M, A, P, G, C, T or S;
- $[X_i]_n$  is a sequence of n amino acids wherein n is from 1 to 50 amino acids

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and wherein the sequence  $X_i$  may comprise the same or different amino acids selected from any amino acid residue;

$X_{17}$  is L, I, V, M, A or P;

$X_{18}$  is any amino acid;

$X_{19}$  is any amino acid;

$X_{20}$  L, I, V, M, A or P;

$X_{21}$  is P;

$X_{22}$  is L, I, V, M, A, P or G;

$X_{23}$  is P or N;

$[X]_n$  is a sequence of n amino acids wherein n is from 1 to 50 amino acids and wherein the sequence  $X_j$  may comprise the same or different amino acids selected from any amino acid residue;

$X_{24}$  is L, I, V, M, A or P;

$X_{25}$  is any amino acid;

$X_{26}$  is any amino acid;

$X_{27}$  is Y or F; and

$X_{28}$  is L, I, V, M, A or P.

22. An isolated protein according to claim 21 wherein the protein modulates signal transduction.

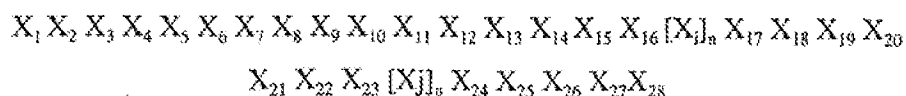
23. An isolated protein according to claim 22 wherein the signal transduction is modulated by a cytokine or other endogenous molecule, a hormone, a microbe or a microbial product, a parasite, an antigen or other effector molecule.

24. An isolated protein according to claim 23 wherein the protein modulates cytokine-mediated signal transduction.

25. An isolated protein according to claim 24 wherein the signal transduction is mediated by one or more of the cytokines EPO, TPO, G-CSF, GM-CSF, IL-3, IL-2, IL-4, IL-7, IL-13, IL-6, LIF, IL-12, IFN $\gamma$ , TNF $\alpha$ , IL-1 and/or M-CSF.

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26. An isolated protein according to claim 25 wherein the signal transduction is mediated by one or more of IL-6, LIF, OSM, IFN- $\gamma$  and/or thrombopoietin.
27. An isolated protein according to claim 26 wherein the signal transduction is mediated by IL-6.
28. An isolated protein according to claim 16 wherein said protein comprises an amino acid sequence substantially as set forth in SEQ ID NO. 4, SEQ ID NO. 6, SEQ ID NO. 8, SEQ ID NO. 10, SEQ ID NO. 12, SEQ ID NO. 14, SEQ ID NO. 18, SEQ ID NO. 21, SEQ ID NO. 25, SEQ ID NO. 29, SEQ ID NO. 36, SEQ ID NO. 41, SEQ ID NO. 44, SEQ ID NO. 46 or SEQ ID NO. 48 or an amino acid sequence having at least about 15% similarity to all or part of the listed sequences.
29. An isolated protein according to claim 16 wherein the said protein is encoded by a nucleotide sequence substantially as set forth in SEQ ID NO. 3, SEQ ID NO. 5, SEQ ID NO. 7, SEQ ID NO. 9, SEQ ID NO. 11, SEQ ID NO. 13, SEQ ID NO. 15, SEQ ID NO. 16, SEQ ID NO. 17, SEQ ID NO. 20, SEQ ID NO. 22, SEQ ID NO. 23, SEQ ID NO. 24, SEQ ID NO. 26, SEQ ID NO. 27, SEQ ID NO. 28, SEQ ID NO. 30, SEQ ID NO. 31, SEQ ID NO. 32, SEQ ID NO. 33, SEQ ID NO. 34, SEQ ID NO. 35, SEQ ID NO. 37, SEQ ID NO. 38, SEQ ID NO. 39, SEQ ID NO. 40, SEQ ID NO. 42, SEQ ID NO. 43, SEQ ID NO. 45 or SEQ ID NO. 47 or a nucleotide sequence having at least 15% similarity to all or a part of the listed sequences or a nucleotide sequence capable of hybridizing to the listed sequences under low stringency conditions at 42°C.
30. An isolated protein or a derivative, homologue, analogue or mimetic thereof having the following characteristics:
- (i) comprises a SOCS box in its C-terminal region wherein said SOCS box comprises the amino acid sequence:



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wherein:

- $X_1$  is L, I, V, M, A or P;
- $X_2$  is any amino acid residue;
- $X_3$  is P, T or S;
- $X_4$  is L, I, V, M, A or P;
- $X_5$  is any amino acid;
- $X_6$  is any amino acid;
- $X_7$  is L, I, V, M, A, F, Y or W;
- $X_8$  is C, T or S;
- $X_9$  is R, K or H;
- $X_{10}$  is any amino acid;
- $X_{11}$  is any amino acid;
- $X_{12}$  is L, I, V, M, A or P;
- $X_{13}$  is any amino acid;
- $X_{14}$  is any amino acid;
- $X_{15}$  is any amino acid;
- $X_{16}$  is L, I, V, M, A, P, G, C, T or S;
- $[X]_n$  is a sequence of n amino acids wherein n is from 1 to 50 amino acids and wherein the sequence  $X_i$  may comprise the same or different amino acids selected from any amino acid residue;
- $X_{17}$  is L, I, V, M, A or P;
- $X_{18}$  is any amino acid;
- $X_{19}$  is any amino acid;
- $X_{20}$  L, I, V, M, A or P;
- $X_{21}$  is P;
- $X_{22}$  is L, I, V, M, A, P or G;
- $X_{23}$  is P or N;
- $[X]_n$  is a sequence of n amino acids wherein n is from 1 to 50 amino acids and wherein the sequence  $X_j$  may comprise the same or different amino acids selected from any amino acid residue;
- $X_{24}$  is L, I, V, M, A or P;
- $X_{25}$  is any amino acid;

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X<sub>26</sub> is any amino acid;

X<sub>27</sub> is Y or F;

X<sub>28</sub> is L, I, V, M, A or P; and

- (ii) comprises at least one of an SH2 domain, WD-40 repeats and/or ankyrin repeats or other protein:molecule interacting domain in a region N-terminal of the SOCS box; and
- (iii) modulates signal transduction.

31. A method of modulating levels of a SOCS protein in a cell said method comprising contacting a cell containing a SOCS gene with an effective amount of a modulator of SOCS gene expression or SOCS protein activity for a time and under conditions sufficient to modulate levels of said SOCS protein.

32. A method of modulating signal transduction in a cell containing a SOCS gene comprising contacting said cell with an effective amount of a modulator of SOCS gene expression or SOCS protein activity for a time sufficient to modulate signal transduction.

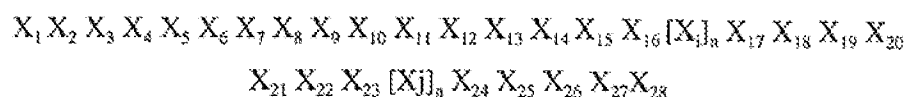
33. A method of influencing interaction between cells wherein at least one cell carries a SOCS gene, said method comprising contacting the cell carrying the SOCS gene with an effective amount of a modulator of SOCS gene expression or SOCS protein activity for a time sufficient to modulate signal transduction.

34. A method according to any one of claims 31-33 wherein signal transduction is mediated by a cytokine, a hormone, a microbe or a microbial product, a parasite, an antigen or other effector molecule.

35. A method according to claim 34 wherein the cytokine is one or more of EPO, TPO, G-CSF, GM-CSF, IL-3, IL-2, IL-4, IL-7, IL-13, IL-6, LIF, IL-12, IFN $\gamma$ , TNF $\alpha$ , IL-1 and/or M-CSF.

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36. A method according to claim 35 wherein the cytokine is one or more of IL-6, LIF, OSM, IFN- $\gamma$  and/or thrombopoietin.
37. A method according to claim 36 wherein the cytokine is IL-6.
38. A method according to any one of claims 31-37 wherein the SOCS gene encodes a protein having a SOCS box comprising the amino acid sequence:



wherein:

- $X_1$  is L, I, V, M, A or P;
- $X_2$  is any amino acid residue;
- $X_3$  is P, T or S;
- $X_4$  is L, I, V, M, A or P;
- $X_5$  is any amino acid;
- $X_6$  is any amino acid;
- $X_7$  is L, I, V, M, A, F, Y or W;
- $X_8$  is C, T or S;
- $X_9$  is R, K or H;
- $X_{10}$  is any amino acid;
- $X_{11}$  is any amino acid;
- $X_{12}$  is L, I, V, M, A or P;
- $X_{13}$  is any amino acid;
- $X_{14}$  is any amino acid;
- $X_{15}$  is any amino acid;
- $X_{16}$  is L, I, V, M, A, P, G, C, T or S;
- $[X_i]_n$  is a sequence of n amino acids wherein n is from 1 to 50 amino acids and wherein the sequence  $X_i$  may comprise the same or different amino acids selected from any amino acid residue;
- $X_{17}$  is L, I, V, M, A or P;
- $X_{18}$  is any amino acid;

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X<sub>19</sub> is any amino acid;

X<sub>20</sub> L, I, V, M, A or P;

X<sub>21</sub> is P;

X<sub>22</sub> is L, I, V, M, A, P or G;

X<sub>23</sub> is P or N;

[X]<sub>n</sub> is a sequence of n amino acids wherein n is from 1 to 50 amino acids and wherein the sequence X<sub>j</sub> may comprise the same or different amino acids selected from any amino acid residue;

X<sub>24</sub> is L, I, V, M, A or P;

X<sub>25</sub> is any amino acid;

X<sub>26</sub> is any amino acid;

X<sub>27</sub> is Y or F; and

X<sub>28</sub> is L, I, V, M, A or P.

39. A method according to claim 38 wherein the SOCS gene comprises a nucleotide sequence selected from SEQ ID NO. 3, SEQ ID NO. 5, SEQ ID NO. 7, SEQ ID NO. 9, SEQ ID NO. 11, SEQ ID NO. 13, SEQ ID NO. 15, SEQ ID NO. 16, SEQ ID NO. 17, SEQ ID NO. 20, SEQ ID NO. 22, SEQ ID NO. 23, SEQ ID NO. 24, SEQ ID NO. 26, SEQ ID NO. 27, SEQ ID NO. 28, SEQ ID NO. 30, SEQ ID NO. 31, SEQ ID NO. 32, SEQ ID NO. 33, SEQ ID NO. 34, SEQ ID NO. 35, SEQ ID NO. 37, SEQ ID NO. 38, SEQ ID NO. 39, SEQ ID NO. 40, SEQ ID NO. 42, SEQ ID NO. 43, SEQ ID NO. 45 or SEQ ID NO. 47.

40. A method according to claim 38 wherein the SOCS gene encodes a protein comprising an amino acid sequence substantially as set forth in SEQ ID NO. 4, SEQ ID NO. 6, SEQ ID NO. 8, SEQ ID NO. 10, SEQ ID NO. 12, SEQ ID NO. 14, SEQ ID NO. 18, SEQ ID NO. 21, SEQ ID NO. 25, SEQ ID NO. 29, SEQ ID NO. 36, SEQ ID NO. 41, SEQ ID NO. 44, SEQ ID NO. 46 or SEQ ID NO. 48.



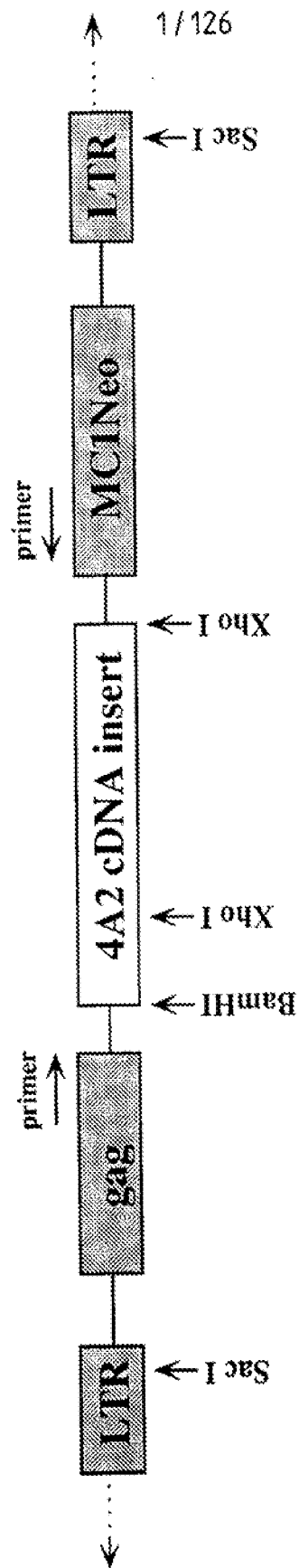


FIGURE 1

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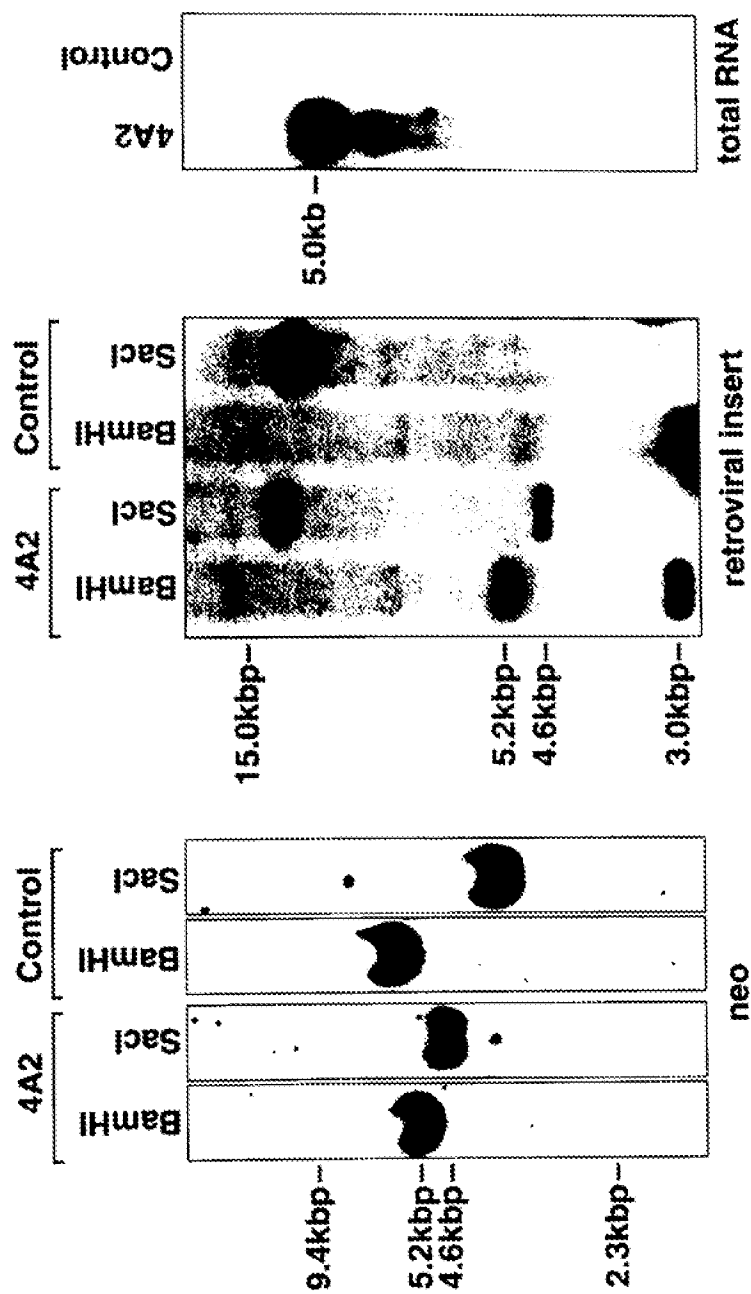
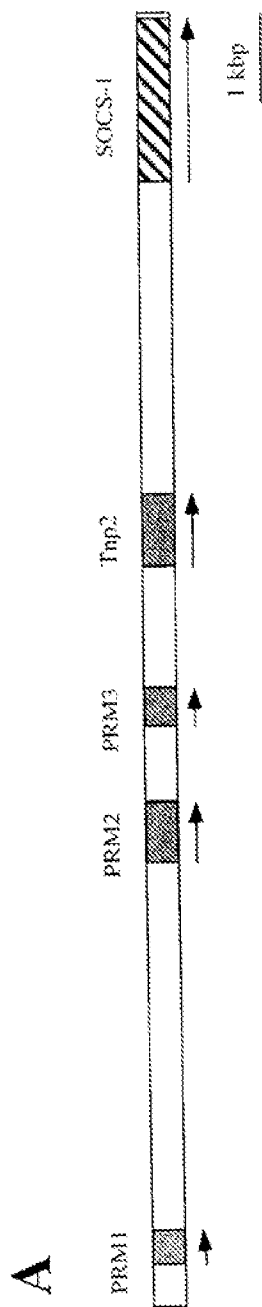


FIG 2

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**FIG 3A**

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-159 cgagggtcaagctccgggaggattctgcgtgccggtctctg  
 -120 ctcttgggggtctgttgccggcctgtgcccacccggagcccggtcactgcctctgtct  
 -60 ccccatcagcgcagcccgaggcctatggcccacccctccagctggccctctgagtagg

1 M V A R N Q V A A D N A I S P A A E P R  
 1 ATGGTAGCACCAACCAGCTGGCAGCCGACAATGGGATCTCCCCGGCAGCAGAGCCCCGA

21 R R S E P S S S S S S S S P A A P V R F  
 61 CGGCGGTTCAGAGCCCTCCTGCTCTCTGTTCTGTCCTGCGCCAGCGCCCCCGTGCCTCCC

41 R P C P A V P A P A P G D T H F R T P E  
 121 CCGCCCTGCCCCGGCGTCCCAGCCCCAGCCCTGGCGGACACTCACTTCGCGACCTTCGCG

61 S H S D V R R I T R T S A L L D A C G F  
 181 TCCCACTCCGATTACCGCGCATCACGCGGACCAGCGCGCTCCTGACGCGCTCGCGCTTC

81 Y W G P L S V H G A H E R L R A E P V G  
 241 TATTGGGGACCCCTGAGCGTGCACGGGCGGCACGAGCGCGCTGCCTGCCGAGCCCGTGGGC

101 T F L V R D S R Q R N C F F A L S V K M  
 301 ACCTTCTTGGTGGCGGACAGTCTCAACCGAACTCCTTCTTCGCGCTCAGCGTGAAGATG

121 A S G P T S I R V H F Q A G R F H L D G  
 361 GCTTCGGGGCCCCACGAGCATCCGCGTGCACCTTCCAGGCCGCGCGCTTCCACTTGGACGGC

141 S R E T F D C L F E L L E H Y V A A P R  
 421 AGCCGCGAGACCTTCGACTGCCCTTTTCGAGCTGCTGGAGCACTACGTGGCGGCGCCCCGC

161 R M L G A P L R Q R R V R P L Q E L C R  
 481 CGCATGTTGGGGGCCCCGCTGCCCGCAGCGCGCGTGGCGCGCTGCAGGAGCTGTGTGCG

181 Q R I V A A V G R E N L A K I P L N P V  
 541 CAGCGCATCGTGGCCCCCGTGGGTGGCGGAGAACCTGGCGCGCATCCCTCTTAACCCGTA

201 L R D Y L S S F P F Q I \*  
 601 CTCCGTGACTACCTGAGTTCCCTTCCCTTCCAGATCTgacccggctgccgctgtgcccag

661 catlaagtgggggcgccttattatttcttattatttattattattatttttctggaacca  
 721 cgtgggagccctccccgcctgggtcggagggagtgttgtggagggtgagatgcctccca  
 781 ctctgggtggagacctcatccacctctcaggggtgggggtgctccctcctgggtgtc  
 841 cctccgggtccccctggttgttagcagcttgtgtctggggccaggacctgaattccactc  
 901 ctacctctccatgtttacataattccagtatctttgcacaaaccaggggtccggggagggt  
 961 ctctggcttcatttttctgtgtgcagaatatctattttatatttttacagccagttta  
 1021 ggtatataaaactttattatgaaagtttttttttaaaagaaaaa

FIG 3B

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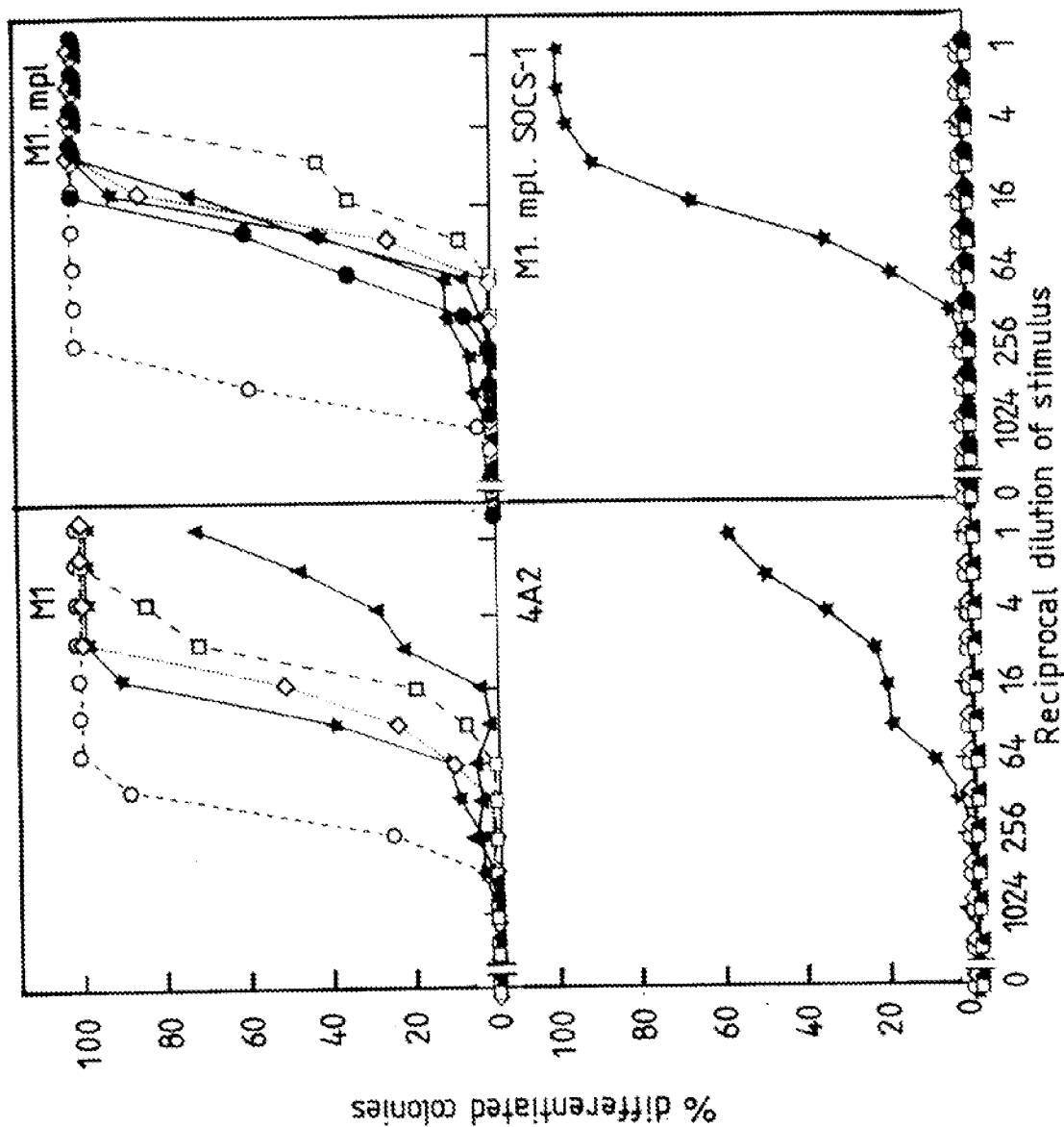


FIG 4

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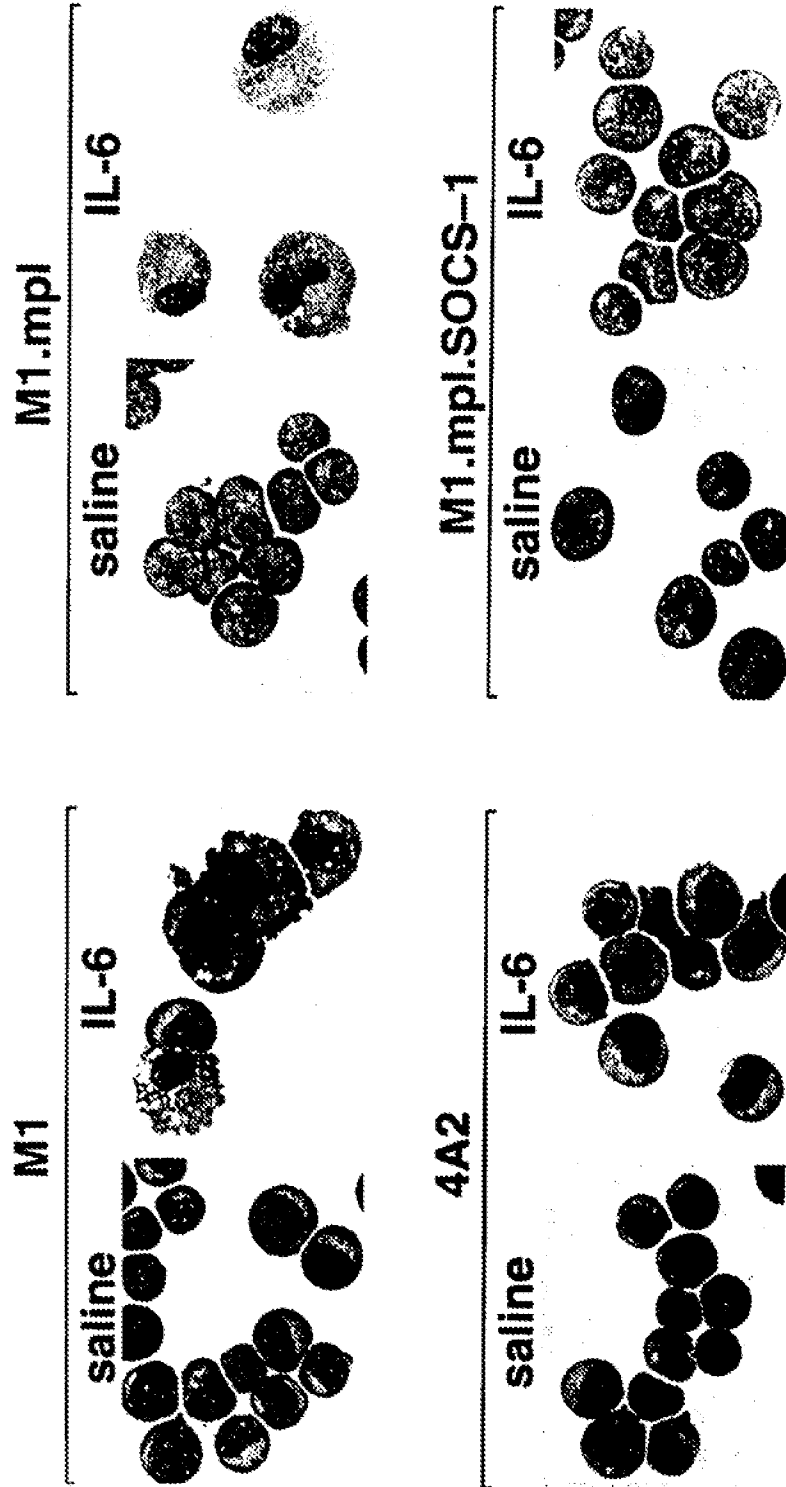
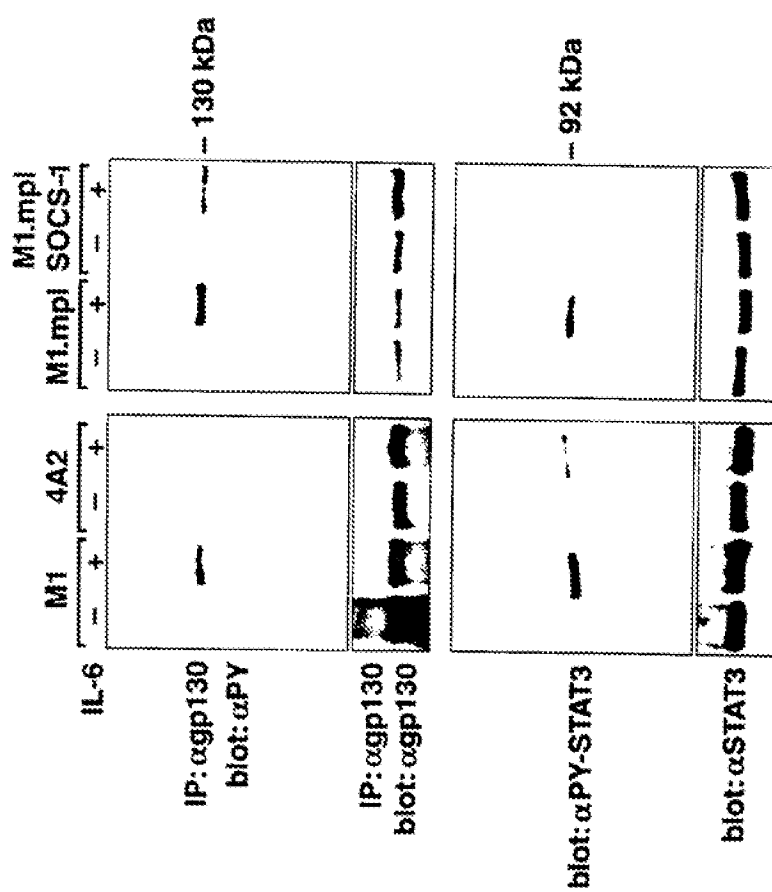


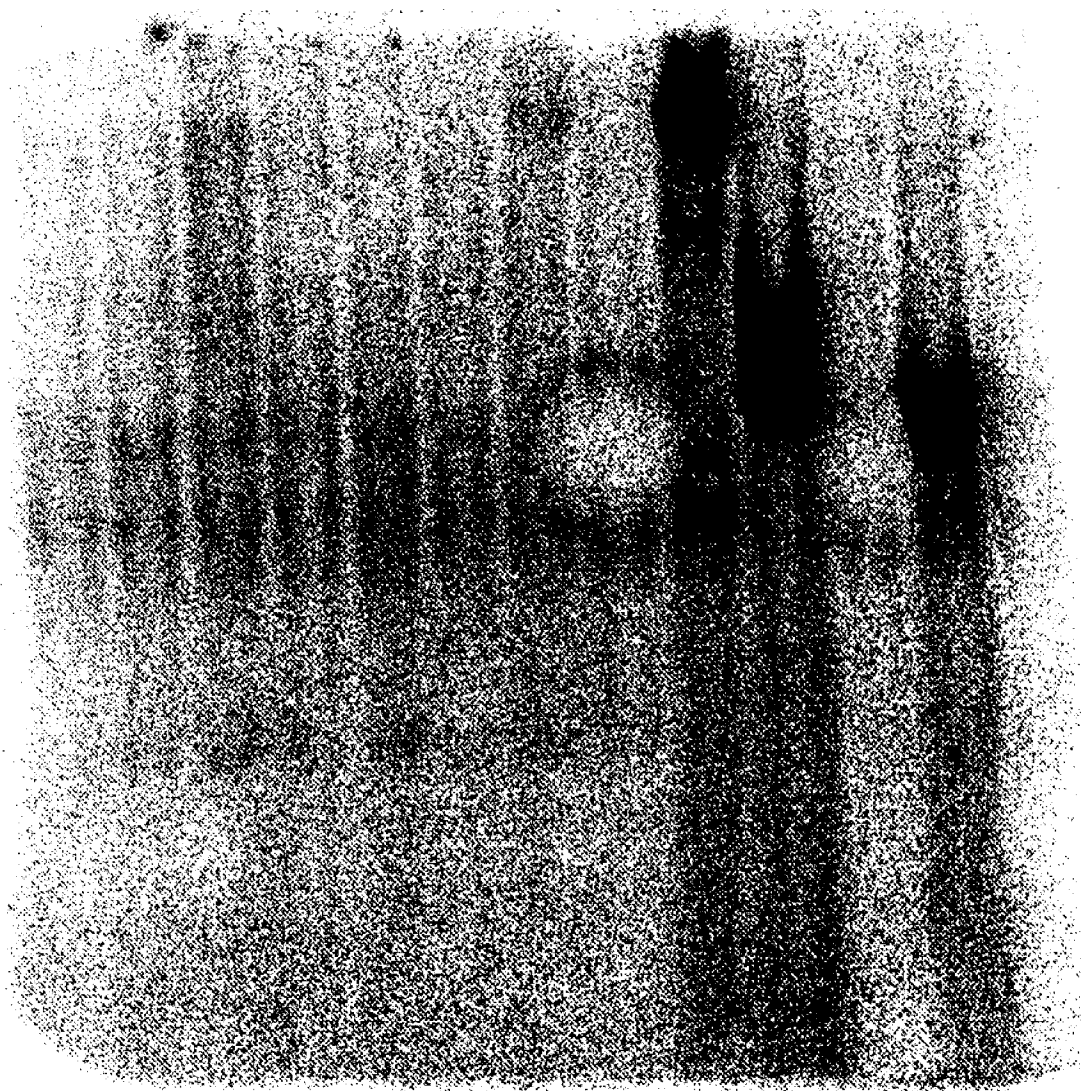
FIG 5

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FIG 6

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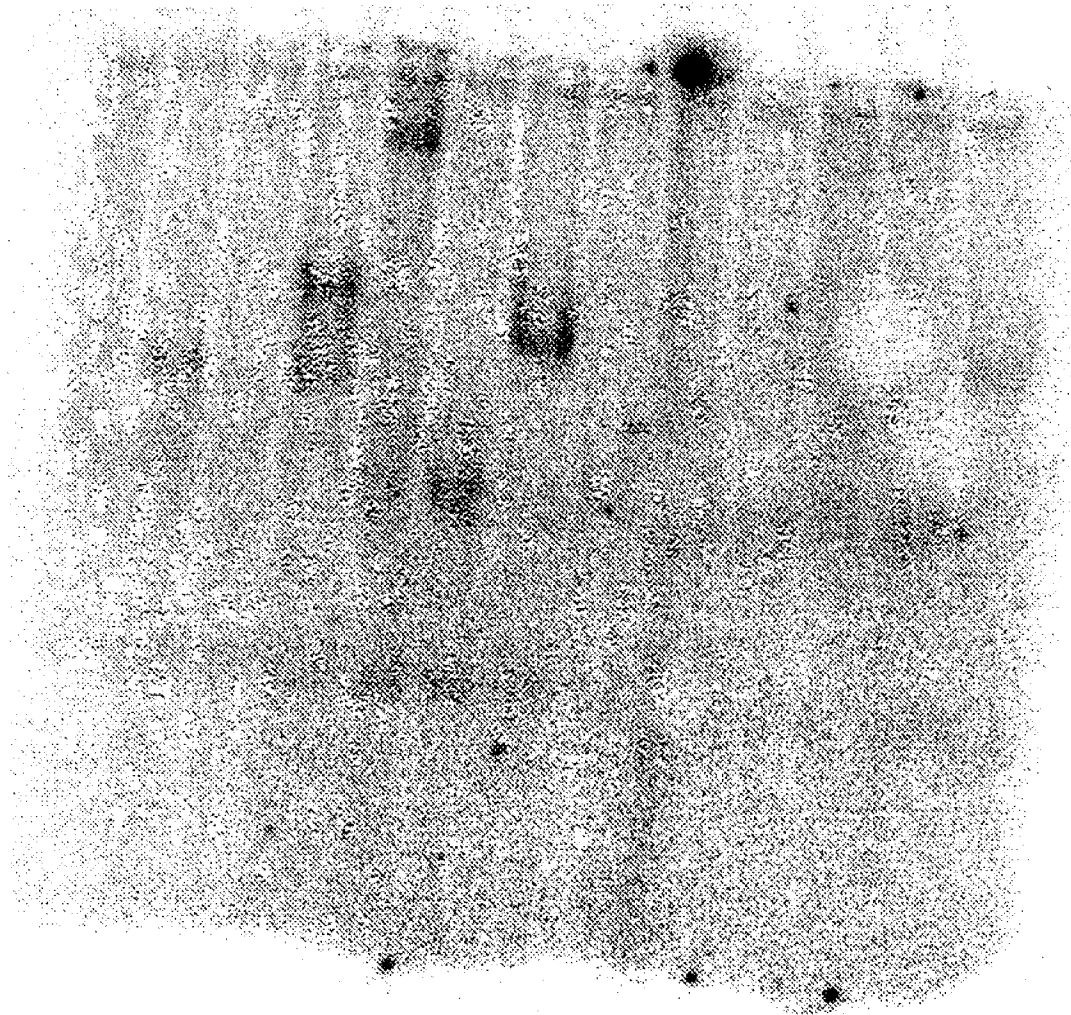
FIG 7A

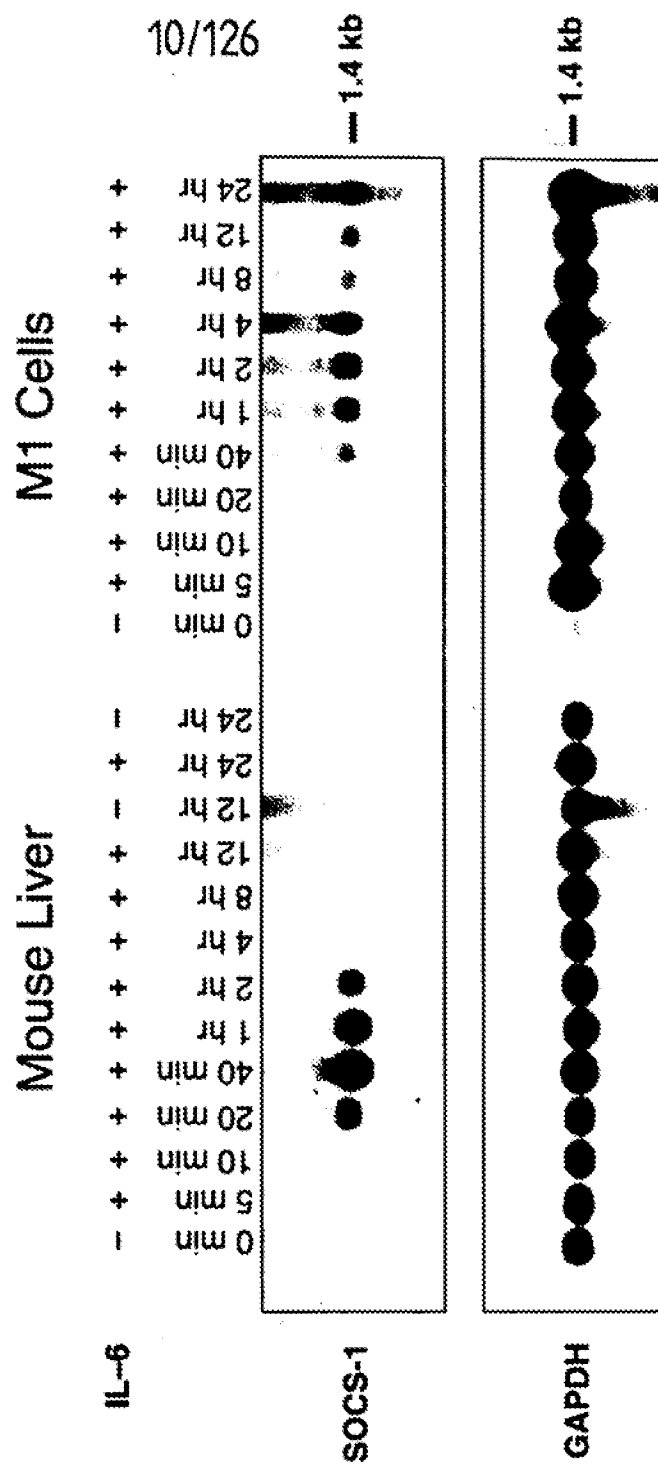




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FIG 7B





FILE 8

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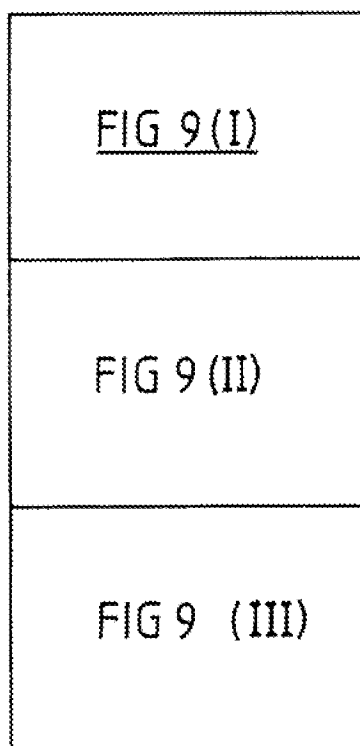


FIG 9





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[illegible]

hs SOCS-1 (193)	V L R D V Y L S S F P F Q I *	(211)
hr SOCS-1 (200)	V L R D V Y L S S F P F Q I *	(212)
mm SOCS-1 (200)	V L R D V Y L S S F P F Q I *	(212)
mm SOCS-2 (186)	R L K R V Y L E E Y K F D V *	(198)
mm SOCS-3 (214)	I R E F L D Q Y D A P L *	(225)
		(257)

FIG 9(III)

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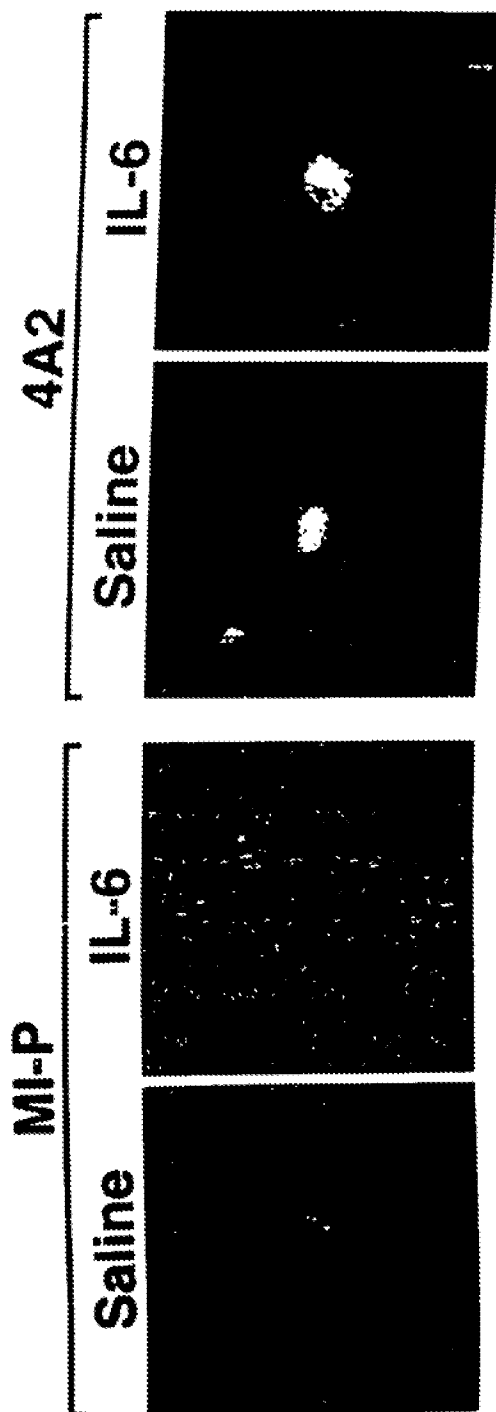
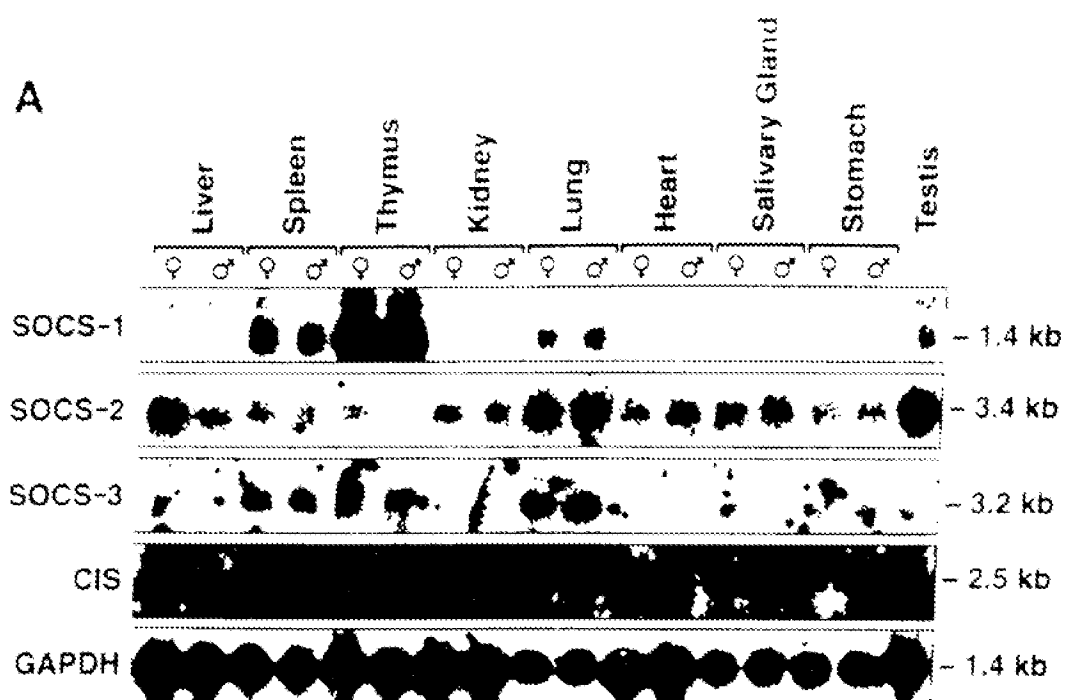


FIG 10

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FIG 11A



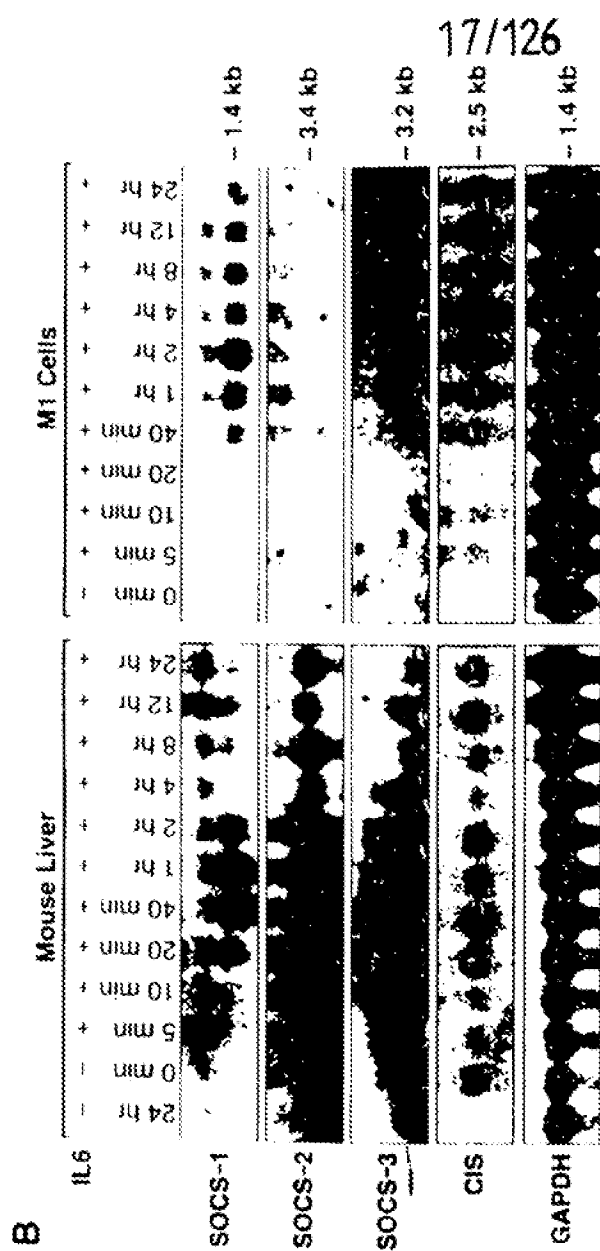


FIG 11B

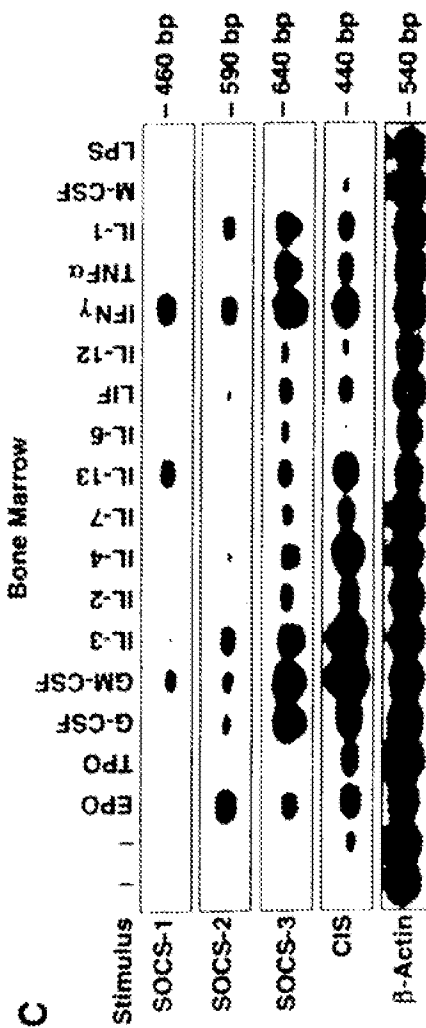


FIG 11C

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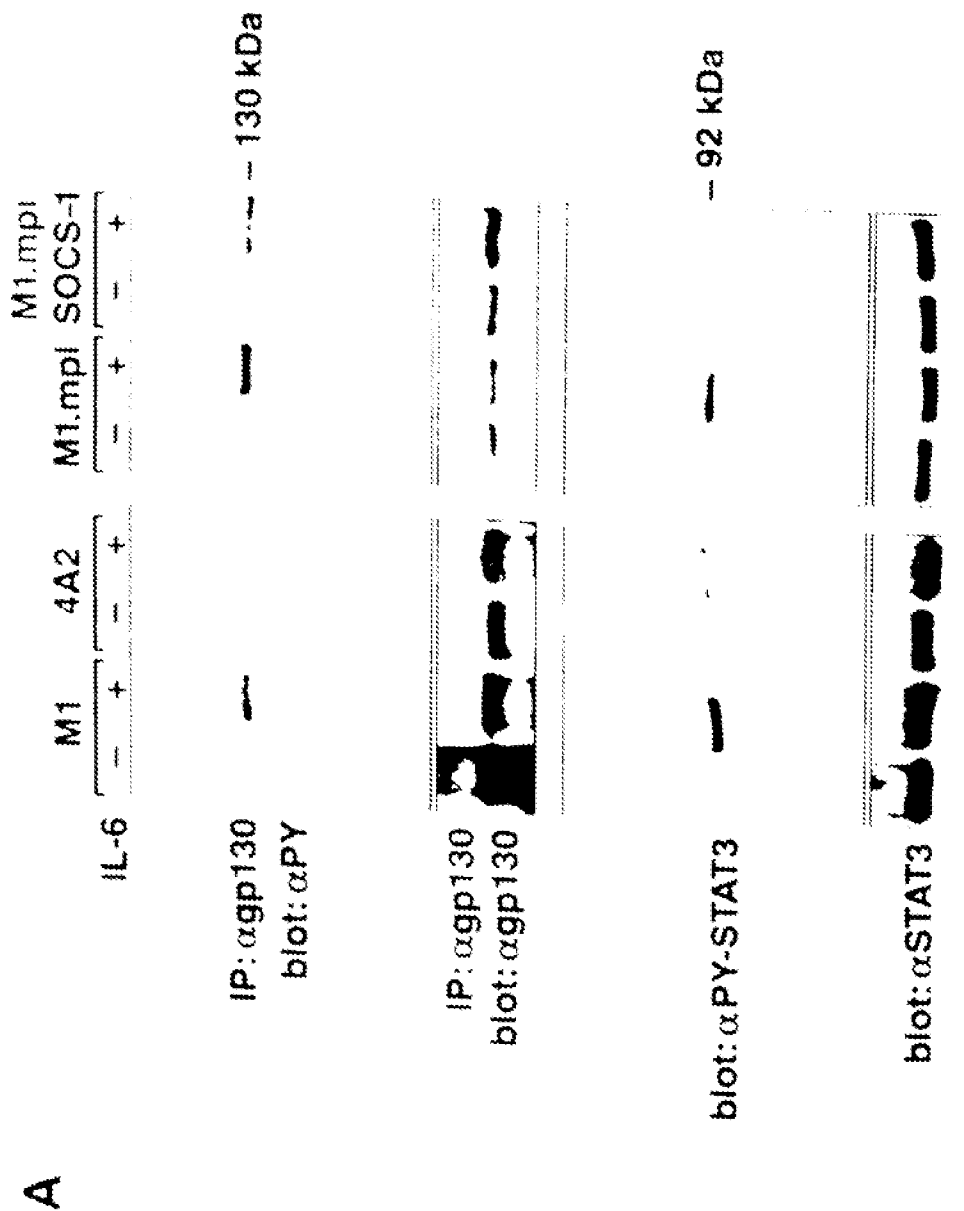


FIG 12A

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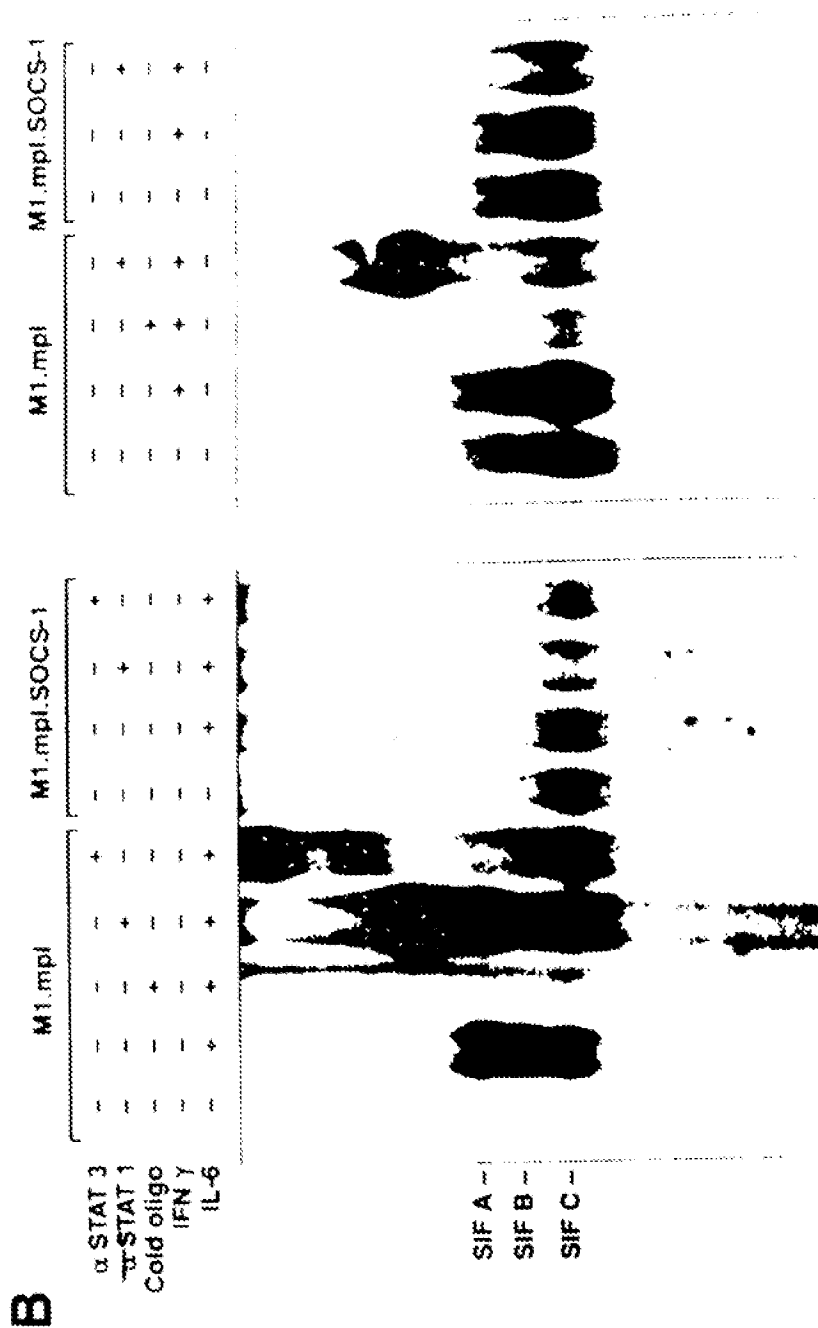


FIG 12B

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FIG 13A(i)	FIG 13A(ii)
FIG 13B(i)	FIG 13B(ii)
FIG 13 C(i)	FIG 13 C (ii)
FIG 13 D	
FIG 13E(i)	FIG 13E(ii)
FIG 13 F (i)	FIG 13F(ii)

FIG 13

SUBSTITUTE SHEET (RULE 26)